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OM protein protein search, using sw. model

Run on: April 29, 2001, 06:40:29; Search time 14.58 Seconds (without alignments) 608.042 Million cell updates/sec

Scoring table: US-09-726-899-3
678
1 MSFPKYKPSSLRTLPETLDP......DRKEKLIQEGKLDRTFHLSY 129

Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

198801 seqs, 68722935 residues

Searched:

number of hits satisfying chosen parameters:

198801

RESULT

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_67:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7			4	ω	2	1	NO.	Result	
67 .	67	67	67	67.5	67.5	7.	7.	89	68	68.5	68.5	•		68.5	69	69	69	69.5	70	70	70.5	74	74	88.5	. 149	315	514	678	Score		
9.9	9.9	•	9.9	•	10.0	10.0	10.0	10.0	10.0	10.1	10.1	10.1	10.1	10.1	10.2	10.2	10.2	10.3	10.3	•	•	10.9		13.1	22.0	46.5	75.8	100.0	Match		90
455	316	232	194	600	296	289	153	716	185	1333	1330	574	294	294	1660	1023	298	294	1025	695	788	451	308	1078	179	133	129	129	Length [
2	2	N	2	2	2	N	ب	ш	N	N	2	ν	N	N	N	N	N	N	2	N	2	N	Ν	2	N	2	N	ν,	BIG		
S71344	T21180	B75121	A82072	C83142	C82645	E75391	MMVQBY	JC5061	S12205	T38401	A36373	S57072	T49271	S23095	T18561	S12519	S69523	S22440	T18376	G64327	S75209	F75177	G83104	S77162	A33164	JC2003	S28237	JE0383	ID		
purinergic recepto		hypothetical prote	7	hypothetical prote	transcription regu	conserved hypothet	genome-linked prot	macrophage-stimula	hypothetical prote	retrotransposable		hypothetical prote		protein kinase (EC		glutactin - fruit	hypothetical prote	protein kinase (EC	multidrug resistan	H+-transporting AT	dnaK protein - Syn	tryptophan synthas	probable ferredoxi	DNA topoisomerase	hypothetical prote	NADH ubiquinone ox	NADH dehydrogenase	NADH dehydrogenase	Description		

alpha-qlucan synth	T43432	2	2371	9.7	65.5	45
probable alpha-glu	T39569	N	2358	9.7	65.5	44
glycine cleavage	D83339	N	959	9.7	65.5	43
nikB protein - Esi	в38529	2	899	9.7	65.5	42
hypothetical prote	T22108	N	354	9.7	65.5	41
RNA14 protein - ye	S54561	ν	677	9.7	66	40
major core protein	FOVZFV	٠.,	657	9.7	66	39
tRNA (5-methylamin	H75357	N	413	9.7	66	38
hypothetical prote	F83570	N	353	9.7	66	37
conserved hypothet	D71324	N	342	9.7	66	36
hypothetical prote	T24965	N	271	9.7	66	ω 5
probable outer men	н81874	2	193	9.7	66	34
preprotein transic	A57386	N	1036	9.8	66.5	ω
Ca2+-transporting	S32230	N	674	9.8	66.5	32
hypothetical prote	E83263	N	634	9.8	66.5	31
methyl viologen-re	В37777	N	472	9.8	66.5	30

ALIGNMENTS

Db	• Oy	Db	Qy	Db	Qy	ма Ма	n Qu
121 LDRTFHLSY 129	121 LDRTFHLSY 129	61 ENPALLRWAYARTINYYPNERDTPKNSLMGALCGEGPLIFIYYIIKTERDRKEKLIQEGK 120	61 ENPALLRWAYARTINVYPNFRPTPKNSLMGALCGFGPLIFIYYIIKTERDRKEKLIQEGK 120	MSFPKYKPSSLATLPETLDPAEYNISPETRRAQAERLAIRAQLKREYLLQYNDPNRRGLI 60	1 MSFPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLKREYLLQYNDBNRRGLI 60	Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match 100.0%; Score 678; DB 2; Length 129;

C;Accession: S28237 R;Walker, J.E.; Arizmendi, J.M.; Dupuis, A.; Fearnley, I.M.; Finel, M.; Medd, S.M.; P. J. Mol. Biol. 226, 1051-1072, 1992 A;Title: Sequences of 20 subunits of NADH: ubiquinone oxidoreductase from bovine hear A;Reference number: S28237; MUID:92389317 A;Accession: S28237 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-129 <WAL> NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain B15 - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999 A;Cross-references: EMBL:X64898; NID:g113; PIDN:CAA46107.1; PID:g114 C;Keywords: electron transfer; mitochondrion; NAD; oxidoreductase

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R;Goldberg, G.S.; Kaczmarczy, ...
Gene 13, 233-235, 1993
A;Title: A chicken genomic DNA fragment that hybridizes to A;Reference number: JC2003; MUID:94040816
A;Accession: JC2003
A;Accession: JC2003
Gene 121,
A;Title:
                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Gallus gallus (chicken)
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 21-Jul-2000
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JC:

NADH ubiquinone oxidoreductase B15 chain li

N;Alternate names: murine Hox-3,1 homeobox
                                A; Experimental source: strain Leghorn R; Goldberg, G.S.; Kaczmarczyk, W. Gene 121, 397-398, 1992
                                                                                                                                                                                                                                                A; Reference number: A33164
A; Accession: A33164
                                                                                                                                                                                                                                                                                                                                                 C;Accession: A33164; JC1395
R;Goldberg, G.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein walter - chicken N; Alternate names: homeotic protein Hox-3.1 homolog; hypothetical 13.1K protein
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A;Introns: 67/3
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A; Residues: 1-133
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                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-179 <GOL>
                                                                                                                                                                                                        A; Status: preliminary; not compared with
                                                                                                                                                                                                                                                                                                                        submitted
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       Sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the Protein Sequence Database,
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novel chicken genomic DNA fragment that hybridizes to the murine
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Pred. No. 2.5e-26;
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                                                                                                                                                                     A;Title: Complete genome sequence of Pseudomonas A;Reference number: A82950; MUID:20437337 A;Accession: G83104
                                                                                                                                                                                                                                                                                C;Accession: G83104
C;Accession: G83104
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, adman, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable ferredoxin reductase PA4331 [imported] - Pseudomonas aeruginosa (str&in C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                             A; Molecule type: DNA
A; Residues: 1-308 <STO>
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   A; Experimental source: strain
                                   A; Cross-references:
                                                                                                                                    A; Status: preliminary
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GB:AE004849; GB:AE004091;

NID:g9950550;

PIDN: AAG07719.1;

GSPDB:GN

aeruginosa PA01,

an

opportunistic

рa

M.J.;

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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S7-162
C;Accession: S7-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
S77162
                                                                                                                                                                                                                                        A;Gene: gyrB
A;Start codon: GTG
C;Keywords: isomer
                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S74322; MUID:97061201 A; Accession: S77162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; W DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: JC1395
A;Molecule type: DNA
A;Residues: 1-124 <GO2>
A;Cross-references: GB:
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                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL:D90908; GB:AB001339; A; Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-1078
                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Sequence analysis of the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA topoisomerase (ATP-hydrolyzing) N;Alternate names: DNA gyrase chain
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755 KEQWTPEFREKREALAQT-
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                                     74 INVY-PNFRPTPKNSLMGALCGFGPLIFIYYIIKTERDRKEKLIQEGKLDRTFHLSY 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EYNISPETRRAQAERL-----AIRAQLKREYLLQYNDPNRRGLIENPALLRWAYART 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYRPNRYVSLPAELDPATYDTPLEKRRAEAERLAIRARLKRQYLLQLNTP
                                                                        EYWAQAENRTAQAERVRQHFAQNPGLRQQYSENAVKQWN-----NPELLKWRQKKT 754
                                                                                                                                                                                                                                              isomerase
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                                                                                                                                                                  13.1%; 28.2%;
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                                                                                                                                                                  Score 88.5; D
Pred. No. 0.4;
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Pred. No. 1.6e-08;
Mismatches 1;
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                                                                                                                                                  Mismatches
YYRKTLAALKQVEIENGYLDISAYDSY 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIDN:AAA70193.1; PID:g211949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wada,
                                                                                                                                                                                                                                                                                                                  NID:g1652725; PIDN:BAA17720.1; to the EMBL Data Library, June
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                                                                                                                                                                                     Length 1078;
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1996
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dnaK protein - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sll1932
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000 C;Accession: S75209
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; A. O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamfada DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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                                                                           A; Residues: 1-788 <KAN>
A; Cross-references: EMB
A; Note: the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     망
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: PAB1970
C;Superfamily:
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A;Gene: PA4331
  C; Superfamily:
                    A; Start codon: GTG
                                        A;Gene: dnaK
                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                          A; Reference number: S74322; MUID:97061201 A; Accession: S75209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB49501.1; A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-451 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: F75177
A; Status: preliminary
                                                            C; Genetics:
                                                                                                                                                        A;Status: nucleic acid sequence not shown;
                                                                                                                                                                                                                                 A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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Best Local (
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Best Local Similarity
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Accession: F75177
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Led to the EMBL Data Library, July 1999
Cription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPGELRKLYSKIGRPTPLFRATNLEKLLG
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heat shock protein 70
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de sequence v
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35.7%;
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was submitted
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Pred. No. 2.9;
5; Mismatches 2
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102
                                                                                                                                                      translation not shown
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4.7;
                                                                           NID:g1652127; PIDN:BAA17123.1; PID:g16521 to the EMBL Data Library, June 1996
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Yamada, M.; Yasud
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multidrug resistance protein 2 - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-20
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T18376
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A; Residues: 1-695 <BUL>
- ~~~~-references: GB:U67478; GB:L77117; NID:g1590958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Bla; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1036-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woes, A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanogenic archaeon, Methanococcus jannas, and the complete genome sequence of the methanococcus and the complete genome sequence of the 
C;Genetics:
A;Gene: mdr2
                                                     A;Molecule type: DNA
A;Residues: 1-1025 <RUB>
A;Cross-references: EMBL:U04640; NID:g439853; PID:g439854;
                                                                                                                                                          A;Accession: T18376
A;Status: preliminary; translated
                                                                                                                                                                                                                                     R;Rubio, J.P.; Cowman, A.F.
Exp. Parasicol. 79, 137-147, 1994
A;Title: Plasmodium falciparum: the pfmdr2 protein is
A;Reference number: Z18924; MUID:94333528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Start codon:
C;Keywords: hyd
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A;Accession: G64327
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Best Local Similarity
Matches 29; Conserv
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Best Local Similarity
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23.6%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9;
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                                                                                                                                                                     from
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                     GB/EMBL/DDBJ
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21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation
                                                                    PIDN: AAA21513.1
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A;Tarle: The complete nucleotide sequence of bacteriophage | A;Reference.number: S69503; MUID:96279738
A;Accession: S69523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Gen. Genet. 233, 10-10, 227
A; Title: Isolation and characterization of A; cence number: S22440; MUID:92293101
A; sion: S22440
A; brotus: preliminary
                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-298 <E
                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein 17 - phage HP1
C;Species: phage HP1
C;Date: 06-Dec_1996 #sequence_revision 13-Mar-1997 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S22440
R;Hashimoto, J.; Hirabayashi, T.; Hayano, Y.; Hata,
Mol. Gen. Genet. 233, 10-16, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-294 <HAS>
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C;Superfamily: Kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein kinase (EC 2.7.1.37) cdc2 homolog 1 - rice
C:Species: Oryza sativa (rice)
C:Date: 13-Jan.1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                    Cross-references: EMBL:U24159; NID:g1046235; PIDN:AAB09202.1; PID:g1046244; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 36.2
                                                                                                                                                                                           Matches
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Best Local Similarity 33...
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keywords: ATP; phosphoprotein; phosphotransferase;
 100 FIYYIIKTERDRKEKLIQEGKLDRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 AFPKWQAQDLATIVPTLDPAGLDLLSKMLRYEPNKRITARQALEHEY 286
                                                         68
                                                                                       64
                                                                                                                         30
                                                                                                                                                11 LRTLPETLDPAEY--NISPETRR----AQAERLAIRAQLKRE-YLLQYNDPNRRGLIENP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       500 KNSLLGSVLFIGLTLYIYSTIKITKWRKKIRTKANEMDNYYH
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                                              RAGQYLFT-SIEITPNFRNSGKAYLSGLGVTDSPASVGTTELKFFNAEQKGSVCG-----
                                                                                                                LHEMAETYDPEHYTANLWPEHRRWFNMGQVIELKAEENEKGETQLFAIIAPNKE-LIEYN 88
                                                                                     ALLRWAYARTINVYPNFRPTPKNSL --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFPKYKPSSLRTLPETLDPAEYN-ISPETRRAQAERLAIRAQLKREY 47
                                                                                                                                                                                       l Similarity 26.9
39; Conservative
                                                                                                                                                                                                                                                                                                             1-298 <ESP>
                                                                                                                                                                                     10.2%; Score 69; DB 2; 26.9%; Pred. No. 9.5; tive 14; Mismatches 5
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                                                                                                                                                                                                                    Length 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S.; Ohashi, Y.; Suzuka, I.;
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                                                                                                                                                                                     Indels
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                                                                                 -- MGALCGFGPLI 99
                                                                                                                                                                                                                                                                                                                                                                                               HP1
                                                                                                                                                                                                                                                                                                                                                                                                                           S.D.; Waldman, A.S.;
                                                                                                                                                                                     42;
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T18561
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S12519
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Best Local
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A:Introns: 28/1; 100/3; 171/3; 791/1
A:Note: CEW1-vit-6
C:Superfamily: vitellogenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Winter, C.E.; Penha, C.; Blumenthal, T.

MOl. Biol. Evol. 13, 674-684, 1996
A;Title: Comparison of a vitellogenin gene between two
A;Reference number: Z18974; MUID:96212989
                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-1660 <WIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change
C;Accession: T18561
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Best Local Similarity
Them 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: T18561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vitellogenin vit-6 [similarity] - Oscheius sp.
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C;Species: Drosophila melanogaster
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:x53286; NID:g297084; PIDN:CAA37380.1; PID:g297085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1023 <OLS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ЕМВО J. 9, 1219-1227, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: S12519
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                                            66 LRWAYARTINVYPNFRPTPKNSLMGALCGFG-----PLIFIY--
                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 DPNRRGLIE-NPALLRWAYARTINVYPNFRP----TPKNSLMGALCGFGPLIFIYYIIK 106
                                                                                                                                   YKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLKREYLLQYNDPNRRGLIENPAL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPPKYKPSSLRTLPETLDPAEYNISPETRRAQAE---RLAIRAQLKREYLLQY-----N 52
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PS1131
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                                                                                                                                                                                  Conservative
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-TIFSNDSVLPKEITASLETVFGGEWNKYLAQIGLYQNNLDSVLSKLLQKVE 741
                                                                                                                                                                                                                                                                                                                                                                                  EMBL: U35449; NID: g1515336; PID: g1515337; PIDN: AAB49749.1
                                                                                                                                                                    10.2%; Su
24.8%; Pred
20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.2%;
26.5%;
                                                                                         -KEIRRRVSQSLASIPVEEQKYLESKHKTFNWFNMQSGAT 686
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                                                                                                                                                                                                    Score 69; DB 2;
Pred. No. 81;
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Pred. No. 44;
                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: phosphotransferase; protein kinase; required for G1 to S-phase transition C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein kinase (EC 2.7.1.37) cdc2 - Arabidopsis thaliana
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FEBS Lett 304, 73-77, 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Title: Exon-intron organization of the Arabidopsis thaliana protein kinase genes CDC2a;Reference number: S23095; MUID:92316202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ene 105, 159-165, 1991
;Title: Identification of two cell-cycle-controlling cdc2.gene homologs in Arabidopsis;Reference number: JQ1337; MUID:92039027
;Accession: JQ1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Control of cell division in plants.

Reference MBBL:D10850; NID:g217848; PIDN:BAA01623.1; PID:g217849; PID: Soc. Trans. 20, 80-84, 1992; PITLE: Control of cell division in plants.

Reference number: A48984; MUID:92339744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Residues: 1-294 <FER>;Cross-references: GB:S45387; NID:g257373; PIDN:AAB23643.1;;Experimental source: flower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:X57839; NID:g16218; PIDN:CAA40971.1; PID:g16219; Perreira, P.C.G.; Hemerly, A.S.; Villarroel, R.; Van Montagu, M.; Inze, Inat.Cell 3, 531-540, 1991

Inat.Cell 3, 531-540, 1991

Filtle: The Arabidopsis functional homolog of the p34cdc2 protein kinase.; Reference number: JQ0967; MUID:93005715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Molecule type: mRNA
;Residues: 1-294 <HIF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: sequence extracted from NCBI backbone (NCBIP:109461):
Hirayama, T.; Imajuku, Y.; Anai, T.; Matsui, M.; Oka, A.
ane 105, 159-165, 1991
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Residues: 1-294 <IMA>
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Best Local
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Residues: 1-294 <INZ>
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                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                               2-256/Domain: protein kinase homology <KIN>
10-18/Region: protein kinase ATP-binding motif
33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rons: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ment: The protein is a key component of the eukaryotic cell cycle.
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240 AFPKWKPTDLETFVPNLDPDGVDLLSKMLLMDPTKRINARAALEHEY 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : cdc2
                                                                                                                                                                   Match 10.1%;
Local Similarity 36.2%;
                                                            2 SFPKYKPSSLRTLPETLDPAEYN-ISPETRRAQAERLAIRAQLKREY 47
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                                                                                                                                   Conservative
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                                                                                                                                                                   Score 68.5; DB 2; Pred. No. 11;
                                                                                                                                   Mismatches
                                                                                                                                   21;
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                                                                                                                                                                                                   Length 294;
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Search completed: April 29, 2001, 06:45:36 Job time: 307 sec

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Minimum I Maximum I Result No. Database Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s Searched: Scoring table: Title: Perfect score: OM protein -18 19 20 21 21 22 23 24 24 26 27 27 28 28 30 31 31 number of hits satisfying chosen parameters: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. DB DB Score 673 509 315 88.5 71 68 67.5 67 67 68.5 68.5 69 70. seq protein search, using sw model length: 0 length: 2000000000 Query Match 110.2 110.2 110.2 110.1 110.1 110.1 110.0 13.1 10.5 10.4 10.3 10.3 10.3 BLOSUM62 Gapop 10.0 , US-09-726-899-3 678 April 29, 2001, 06:45:14 ; Search time 9.22 Seconds (without alignments) 479.280 Million cell updates/sec SwissProt_39:* 93435 seqs, 34255486 residues Copyright MSFPKYKPSSLRTLPETLDP.....DRKEKLIQEGKLDRTFHLSY 129 Length 1025 10650 294 1333 270 153 270 153 6155 6157 677 450 2358 1036 654 450 2358 1036 2358 1036 GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd DΒ Gapext 0 SECA_SPIOL
LOLB NEIMA
VP4B_FOWPV
RN14 YEAST
DHE4_LACBI
MOKD_SCHPO
DSBA_BURCE
RSEB_HAEIN
MTHR_MOUSEE
AUJE7_YEAST
AUG_ARTSF
NOS_ANOST
CC2_MAIZE MTHR_HUMAN
GLT_DROME
VIT6_OSCBR
CC2A_ARATH
YJ23_YEAST
RDPO_SCHPO
LPSC_RHIME CC21_ORYSA VPO_BPHP1 SX18_HUMAN VATI_METJA GYRB_SYNY3
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DNK3_SYNY3 NB5M_HUMAN NB5M_BOVIN NB5M_CHICK VPG_BYDVP P2X5_RAT summaries SUMMARIES 93435 P25298 P54388 P54719 Q9y719 Q9rhv8 P44792 Q9wu20 P47050 P35316 061608 P42898 P33438 Q94637 P24101 P247113 Q05654 Q9r9m9 P51571 P51571 Q347215 Q347215 Q347215 P35713 Q57675 P29618 P51719 Q9x3x1 P73098 P48305 P48306 Description 095168 homo sapien 7 oscheius br
0 arabidopsis
0 asaccharomyc
4 schizosacch
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3 barley yell
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2 1 62 61

SFPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLKREYLLQYNDPNRRGLIE 61

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Query Match 99.3%; Best Local Similarity 100.0%; Matches 128; Conservative

Score 673; DB 1; ; Pred. No. 3.7e-63; 0; Mismatches 0;

Length 128;; Indels

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SO SO	388888	388	នននន	CCE	R R R	RX A	R R P	28	888	G DE	DE DI	DT	AC	RESULT NB5M_H								
EMBL; AF MIM; 603 Oxidored INIT_MET MOD_RES SEQUENCE	the Euro use by modified entities or send	€ W →		Biochem. -!- FUNC CHAI	"cDNA of oxidored	MEDL:	[1] SEQUENCE	Mammalia; NCBI_TaxI	Homo	(COMPL	NADH-	15-JU	095168;	RESULT 1 NB5M_HUMAN ID NB5M		5 1	4 4 4 4 W 6	41	40	38	36 37	υ υ • υ
F044 3840 duct	be European Bio by non-pro dified and thi tities require send an email	SWISS-P	TO BE UECATALYTI	hem. Bic FUNCTION CHAIN. 1	"cDNA of eight oxidoreductase:	J 9	ENCE FRO	Mammalia; Euther NCBI_TaxID=9606;	sapiens	(COMPLEX I-B15)	NADH-UBIQUINONE	15-JUL-1999	58;	T 1 HUMAN NB5M_HUMAN		62.5	62. л (л	ر م 93	6 u	3 & 8	63.5 63	
⊅	inf fit s s	SWISS-PROT entry is	TO BE UBIQUINONE. CATALYTIC ACTIVITY: NA SUBUNIT: COMPLEX I IS SUBCELLULAR LOCATION:	them. Biophys. Res. Control of the c	the smeets that nuclear see human		FROM N.A.	Eutheria; D=9606;	Homo sapiens (Human). Eukarvota: Metazoa: (315) (CI	(Rel. 3	(Rel. 3	(BG1 3	STAN			999					
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₹ 50 .	rmatics Institute. To institutions as long atement is not remove license agreement (Selicense@isb-sib.h).	copyright. It is	NADH + IS COMPO N: MITOC	Commun. OF ELECTR	encoded complex I	987855 s R.H.					t anno	Last sequence update	-	יסי			1 AMP					
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chondrion; ARITY. ION (BY SIM	The ong oved.	ht. It is produced through a collaboration -	= NAD(+) JT 40 DIFF	hem. Biophys. Res. Commun. 253:415-422(1998). FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BEL	C.A.F., Smeets K.J.P., Trijbels J.M.F., Smeltink J.A.M.; eight nuclear encoded subunits of NADH:Ubiquinone uctase: human complex I cDNA characterization completed."	n Heuvel		Catarrhini; Hominidae; Homo.	a: Vertebrata: I		<pre>L. 38, Last annotation update) OXIDOREDUCTASE B15 SUBUNIT (EC 1.6.5.</pre>	pdate)		128 AA.	ENTS	H	i A	3 E	ÖĤ	; 4 ;	z ¯	ă F
on	no restricticontent is by and for www.isb-sib.c	through a c	+ UBIQUINOL ERENT SUBUN ANE; MATRIX	RESPIRA NZYME IS	Smeitink J.A.M.; Obiquinone ation completed.	Schuelke M.,		Homo.	anteleos		3) (EC					P06125	P79171	P07668	Q02059	P53830	034526 P44118	005090
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SEQUENCE
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Bos taurus (Bovine).

Eukaryota; Metazoa; C
Mammalia; Eutheria;

Mammalia; Eutheria;
                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE B15 SUBUNIT (EC 1.6.5.3) (EC
                                                                                                                         1 SFPKYEASRLSSLPTTLDPAEYDISSETRKAQAERLAIRSRLKREYQLQYYDPSRRGVIE
                                                                                                                                   2 SFPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLKREYLLQYNDPNRRGLIE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissue-Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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121 DRTFHLSY 128
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CBI_TaxID=9913;
                                                                          DRTFHLSY 129
                                                                                    DPALVRWTYARSANIYPNERPNTKTSLLGALFGIGPLVFWYYVFKTDRDRKEKLIQEGKL 120
                                                          DRTFNISY
                                                                                             NPALLRWAYARTINVYDNERPTPKNSLMGALCGEGPLIFIYYIIKTERDRKEKLIQEGKL 121
                                                                                                                                                                          94;
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          STANDARD;
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                                                                                                                                                                      18;
                                                                                                                                                                          Score 509; DB 1;
Pred. No. 4.1e-46;
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8; Mismatches
                                                                                                                                                                                                             ACETYLATION.
CC1352E9E80DF7D5 CRC64;
         PRT;
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Best Local
                                                               GYRB_SYNY3
P77966;
01-NOV-1997
               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
DNA GYRASE SUBDRIT B (EC 5.99.1.3).
                                                                                                            SYNY3
         GYRB OR SLL2005
                                                                                                                                                                                                                                                                                                                                          EMBL; X60778; CAA43193.1; ALT_SEQ.
EMBL; M84354; AAA70193.1; ALT_SEQ.
Oxidoreductase; NAD; Ubiquinone; M:
SEQUENCE 133 AA; 14938 MW; ED7)
                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the murine Hox-3.1 homeobox.";

Gene 121:397-398(1992).

-1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVE
TO BE UBIQUINONE (BY SIMILARITY).

-1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
-1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERINT SUBUNITS.
-1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE; MATRIX SIDE
                                                                                                                                                                      65 LLRWAYARTINVYPNFRPTPKNSLMGALCGFGPLIFIYYIIKTER
                                                                                                                                                                                                         12 EYRPNRYVSLPAELDPATYDTPLEKRRAEAERLAIRARLKROYLLQLNTPKPPRVIEDPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldberg G.S., Kaczmarczyk W.;
"Sequence of a novel chicken genomic DNA fragment that hybridizes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93077061; PubMed=1359990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDILINE-94040816; PubMed-7901127;
Goldberg G.S., Kaczmarczyk W.;
"A chicken genomic DNA fragment that hybridizes to the murine Hox-3.1 homeobox is likely to encode the NADH ubiquinone oxidoreductase
                                                                                                                                                                                                                                                                                              Loca l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 133:233-235(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P48306;
01-FEB-1996 (Rel. 33, Created)
01-FCT-1996 (Rel. 34, Last sequence update)
15-JUL-1996 (Rel. 34, Last sequence update)
15-JUL-1996 (Rel. 36, Last annotation update)
PUTATIVE NADH-UBIQUINONE OXIDOREDUCTASE B15 SUBUNIT (EC 1.6.5.3)
(EC 1.6.99.3) (COMPLEX I-B15) (CI-B15) (HYPOTHETICAL PROTEIN WALTER)
                                                                                                                                                                                                                         5 KYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLKREYLLQYNDPNRRGLIENPA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                      LLRWDYARTHNYYPTFRPTPKTSFLGAVFAIGPILFWIAAFKTER
                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                          Conservative
                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
                                                                                                                                                                                                                                                                                        46.5%;
                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                  Score 315; DB 1; Pred. No. 6.1e-26;
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                       e; Mitochondrion.
ED7E82948C97B352 CRC64;
                                                                                                                                                                                                                                                                      Mismatches
                           update)
on update)
                                                                                   1078
                                                                                   ĄΑ
                                                                                                                                                                                                                                                                      29;
                                                                                                                                                                                                                                                                                              Length 133;
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(strain PCC 6803)

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Вр
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   AC ID
                                                      FPG_ZYMMO
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                                                                                        RESULT
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Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRO01265; ...
InterPro; IPRO01241; ...
InterPro; IPRO02204; ...
InterPro; IPRO02288; ...
InterPro; IPRO02288; ...
Pfam; PF00986; DNA_gyraseB_C; 1.
Pfam; PF00204; DNA_topoisoII; 2.
FPG_ZYMMO
Q9X3X1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0418; TPIZEAMILY.

PRINTS; PRO1159; DNAGYRASEB.

PROSITE; PS00177; TOPOISOMERASE_II; 1.

PROSITE; PS00881; PROTEIN_SPLICING; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D90908; HSSP; P06982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumu
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria: Cyanobacteria: Chroococcales: Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rotein splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .somerase;
                                                                                                                                                                          755 KEQWTPEFREKRREALAQT--
                                                                                                                                                                                                                                                                                        704
                                                                                                                                                                                                                              74 INVY-PNFRPTPKNSLMGALCGFGPLIFIYYIIKTERDRKEKLIQEGKLDRTFHLSY 129
                                                                                                                                                                                                                                                                                                                                                    22
                                                                                     S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING OF DOUBLE-STRANDED DNA.

SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN AZBZ TETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT A POST-TRANSLATIONAL EXCISION OF THE INTERVENING REGION FOLLOWED BY PEPTIDE LIGATION (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                 EYNISPETRRAQAERL-----AIRAQLKREYLLQYNDPNRRGLIENPALLRWAYART 73
                                                                                                                                                                                                                                                                                        EYWAQAENRTAQAERVRQHFAQNPGLRQQYSENAVKQWN---
                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity 28.3
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Topoisomerase; ATP-binding; Autocatalytic cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       437
872
1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAA17720.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1AJ6
                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436
871
1078
A; 122819
                                                                                                                                                                                                                                                                                                                                                                                                                                13.1%; 28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYRB, 1ST PART (POTENTIAL).
SSP GYRB INTEIN (POTENTIAL).
GYRB, 2ND PART (POTENTIAL).
MW; 6CA02586DFEA607B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                       -YYRKTLAALKQVEIENGYLDISAYDSY 800
                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 0.
                           270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
. 24;
                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1078;
                                                                                                                                                                                                                                                                                        -NPELLKWRQKKT 754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THAT INVOLVES
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                                                                                                                                                                                                                                                                                                                                                                                                           29;
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   RESULT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                          DNK3_SYNY3
P73098;
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                  _SYNY3
"Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                             Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                     Synechocystis sp. (strain Bacteria; Cyanobacteria; NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee H.J., Kang H.S.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-i-FUNCTION: THIS ENZYME MAY PLAY A SIGNIFICANT ROLE IN PROCESSES
-LEADING TO RECOVERY FROM MUTAGENESIS AND/OR CELL DEATH BY
ALKYLATING AGENTS (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: HYDROLYSIS OF THE DEOXYRIBOSE N-GLYCOSIDIC
BOND TO EXCISE 2,6-DIAMINO-4-HYDROXY-5N-METHYLFORMAMIDOPYRIMIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (EC 3.2.2.23) (FAPY-DNA
                                                  Shimpo S.,
Tabata S.;
                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
DNAK PROTEIN 3 (HEAT SHOCK PROTEIN 70) (HSP70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01149; Fapy_DNA_glyco; 1. PROSITE; PS01242; FPG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-ATCC 31821
                                                                                                                                      SEQUENCE FROM N.A. MEDLINE-97061201; PubMed-8905231;
                                                                                                                                                                                                                                       DNAK3 OR SLL1932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA repair; Hydrolase; Glycosidase; Zinc.
ZN_FING 246 268 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF088896; AAD21547.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FAPY) OR 4,6-DIAMINO-5-FORMAMIDOPYRIMIDINE.
-!- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (F.-!- SIMILARITY: BELONGS TO THE FPG FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Sphingomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zymomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTM OR FPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLYCOSYLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 QLKREYLLQYNDPNRRG----LIENPALLRWAYARTINVYP---NFRP
                                                                                                                                                                                                                                                                                                                                                                                                                                    96 QTKNNFIVSLYDPRRFGSLDLVKKNQLLEWSYFRNIGPEPLTGNFNP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 36.:
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 AA;
                                                                                                                                                                                                                                                                                                            (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                         (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / 2M4 / CP4;
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                                                                                                                                                                                                                         PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71; DB : Pred. No. 3.1; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6;
                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EED0E1943D3F5F58 CRC64;
                                                                                                                                                                                                                                                           70) (HSP70)
                                                                                                                                                                                                                                                                                                                                                771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                           Synechocystis
                                                                                                                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
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           SX18_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 3:109-136(1996).
-I- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
-I- INDUCTION: BY STRESS CONDITIONS E.G. HEAT SHOCK (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00301; HEATSHOCK70.

PROSITE; PS00297; HSP70_1; 1.

ROSITE; PS00329; HSP70_2; 1.

ROSITE; PS01036; HSP70_3; FALSE_NEG.

Chaperone; ATP-binding; Multigene family; Heat shock.

SEQUENCE 771 AA; 86030 MW; BE715F28B372738C CRC64;
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Jukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-OCT-2000 (Rel. 40, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
TRANSCRIPTION FACTOR SOX-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SX18_HUMAN
P35713; Q9NPH8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001023; -. Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D90903; BAA17123.1; -. HSSP; P19120; 1ATS.
                                                                                                                                                                      Azuma T., Seki N., Yoshikawa T., "cDNA cloning, tissue expression homolog of SOX18.";
                                                                                                                                                                                                                                                                             PubMed=10858556;
PubMed=10858556;
Stanojcic S., Stevanovic M.;
The human SOX18 gene: cDNA
"The human SOX18 and 1402.
Nucleic Acids Res. 20:2887-2887 (1992).
-1. FUNCTION: BINDS TO THE CONSENSUS SEQUENCE 5'-AACAAAG-3'
ABLE TO TRANS-ACTIVATE TRANSCRIPTION VIA THIS SITE (BY
                                                                                        MEDLINE=92310993; PubMed=1614875; Denny P., Swift S., Brand N., Dab
                                                                                                                                                       Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                         SEQUENCE OF 96-149 FROM N.A
                                                                                                                                                                                                                        TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622
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                                                                                                                                                                                                                                       EQUENCE FROM N.A.
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                                                                nny P., Swift S., Brand N., Dabhade N., conserved family of genes related to t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETLDPAEYNISPETRRAQAERLAIRAQLKREYLLQYNDPNRRGLIENPALLRWAYARTI- 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NVYPNFRPTPKNSLMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.4%;
                                                                                                                                                                                                                                                                    cDNA cloning and high resolution mapping.";
1492:237-241(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 70.5;
pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                      Masuho Y., Muramatsu M. and chromosome mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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                                                                         Barton P., Ashworth i ne testis determining
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                                                                                         Ashworth A.;
                                                                                                                                                                                          of human
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A REAL REPORTS OF THE REAL PROPERTY OF THE REAL PRO
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Best Local Similarity
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                                                                                                                                                   MEDITNE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Claycon R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X65664; CAA46615.1;
PIR; S21482; S21482.
PIR; S22941; S22941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ243896; CAB95835.1; -. EMBL; AB033888; BAA94874.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
V-TYPE ATP SYNTHASE SUBUNIT I (EC 3.6.1.34) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q57675;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR000910; -. Pfam; PF00505; HMG_box; 1.
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                                                                         Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanoco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATPI OR MJ0222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VATI_METJA
                         Science 273:1058-1073(1996)
                                                "Complete genome sequence of jannaschii.";
                                                                                                                                                                                                                                                                                                                                                             STRAIN-JAL-1
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanococcus
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SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
SIMILARITY: CONTAINS 1 HMG BOX.
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  FUNCTION:
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                                                                                                                                                                                                                                                                                                                                                             / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RKKQARKARRLEPGLL 173
  PRODUCES ATP FROM ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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; 327462E519770062 CRC64;
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     PRESENCE
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CC21_ORYSA
ID CC21_ORYSA
AC P29618;
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Best Local
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SEQUENCE
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01-APR-1993 (Rel. 25,
01-OCT-1996 (Rel. 34,
CELL DIVISION CONTROL
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                                                                                                                                 Hashimoto J., Hirabayashi \dot{T}., Hayano Y., Hata S., Ohashi Y., Suzuka I., Utsugi T., Toh-E A., Kikuchi Y., "Isolation and characterization of cDNA clones encoding cdc2 homologues from Oryza sativa: a functional homologue and cognate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                             MEDLINE=92293101; PubMed=1376401;
                                                                                                                                                                                                                                                                                           NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; I
Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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. Gen. Genet. 233:10-16(1992).

FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYOTIC CELL CYCLE. COMPONENT OF THE KINASE COMPLEX THAT PHOSPHORYLATES THE REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II.

ENZYME REGULLATION: PHOSPHORYLATION AT THR-14 OR TYR-15 INACTIVATES THE ENZYME, WHILE PHOSPHORYLATION AT THR-161. ACTIVATES IT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRADIENT ACROSS THE MEMBRANE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FHL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALAQKWEK - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLRWAYARTINVYPNFRPTPKNSLMGALCGFGPLIFIYYIIKTERDRKEKLIQEGKLDRT 124
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Poales; Poaceae; Ehrhartoideae; Oryzeae;
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Pred. No.
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Best Local
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P51719;
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BINDING
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                                                                                                         This SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                     Bacteriophage HP1.
Viruses; dsDNA vir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                        EMBL; U24159; AAB09202.1;
                                               or send an email to license@isb-sib.ch).
                                                          entities requires a license agreement
                                                                                                the European Bioinformatics Institute.
                                                                                                                                                            Nucleic
                                                                                                                                                                                             MEDLINE=96279738; PubMed=8710508; Esposito D., Fitzmaurice W.P., Be
                                                                                                                                                                                                                                                                                               PROBABLE CAPSID SCAFFOLDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed
           Capsid
                                                                       modified and this statement is not removed.
                                                                                                                                              "The complete nucleotide sequence of bacteriophage HP1 DNA."; Nucleic Acids Res. 24:2360-2368(1996).
-i- SIMILARITY: STRONG, TO PHAGE P2 PROTEIN O.
                                                                                                                                                                                    Waldman A.S., Scocca J.J.;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           NCBI_TaxID=10690;
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                                                                                                                                                                                                                                                                                                                                                                                                                      240 AFPKWQAQDLATIVPTLDPAGLDLLSKMLRYEPNKRITARQALEHEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SFPKYKPSSLRTLPETLDPAEYN-ISPETRRAQAERLAIRAQLKREY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S22440; S22440.
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            assembly
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                                                                                                                                                                                                                                                                     dsDNA viruses,
                                                                                  non-profit institutions as long
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Cell division; Mitosis; Phosphorylation
4 287 PROTEIN KINASE.
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34, Last annotation updat
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                                                                                                                                                                                                                                                                     RNA stage; Tailed phages; Myoviridae
                                                                                                                                                                                                                                                                                             PROTEIN (ORF17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 69.5;
Pred. No. 5;
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ATP (BY SIMILARITY).
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                                                                                                                                                                                             Benjamin R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                           298
                                                         noved. Usage by and for (See http://www.isb-sib.
                                                                                                There are no
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                                                                                                                                                                                               Goodman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 294;
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                                                                                                restrictions
                                                                                                                                                                                               S.D.,
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MRI outstation -
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Best Local
gene and genotype/phenotype methylenetetrahydrofolate re
                                                                                         Homberger A., Linnebank M., Winter C., Rapp "Revised translation initiation site of the methylenetetrahydrofolate reductase (MTHFR) submitted (MAR-1999) to the EMBL/GenBank/DDI
                                                                                                                                                                                                                    Goyette P., Pai A.,
                                                                                                                                                                                                                                                                                                                                MEDLINE=95038846; PubMed=7951330;
Goyette P., Summer J.S., Milos R.;
Matthews R.G., Rozen R.;
Nat. Genet. 7:551-551(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                    mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matthews R.G., Rozen R.; "Human methora"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.5.1.20).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32,
15-JUL-1999 (Rel. 38,
01-OCT-2000 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P42898;
                                          Goyette P., Frosst P.,
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  MEDLINE-98345426;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   "cDNA for human methylenetetrahydrofolate Patent number WO9533054, 07-DEC-1995.
                                                                                                                                                                                                                                                                                                                                                                                                         "Human methylenetetrahydrofolate reductase: mapping and mutation identification."; Nat. Genet. 7:195-200(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-415 FROM N.A., AND VARIANT GLN-157
                "Seven novel mutations in the methylenetetrahydrofolate gene and genotype/phenotype correlations in severe
                                                      MEDLINE=95243219; PubMed=7726158;
                                                                   VARIANTS Q-52; M-227; L-251; C-325;
                                                                                                                                                                               "Gene structure of human and mouse (MTHFR).";
                                                                                                                                                                                                                                                                                Rozen R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95004587; PubMed-7920641;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens (Human)
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                                                                                                                                                                  Genome 9:652-656(1998).
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       reductase
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Catarrhini; Hominidae
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                                                                                                                                                                                           methylenetetrahydrofolate reductase
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                                                                                                                                                                                                                                                                                                                                                        Duncan A.M.,
       deficiency."
                                                                   C-335;
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f the
                                          Rozen R.;
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                                                                 C-357,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   isolation of
                                                                                                                    human
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                                                                                                                                Koch
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                                                                   AND
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                                                                                                                                H.G.;
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"Identification of four novel mutations methylenetetrahydrofolate reductase deficur. J. Hum. Genet. 6:257-265(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98213590; PubMed-9545406; Schneider J.A., Rees D.C., Liu Y.-T., Clegg J.B.; "Worldwide distribution of a common methylenetetrahydrofolate reductase mutation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS SER-324 AND GLY-339. MEDLINE-98454315; PubMed-9781030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goyette P., Christensen B., Rosenblatt D.S., Rozen R.; "Severe and mild mutations in cis for the methylenetetrahydrofolate reductase (MTHFR) gene, and description of five novel mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutation in methylenetetrahydrofolate reductase.
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"A candidate genetic risk factor for vascular disease: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT VAL-222
                                                                                                                                                                            -
                                                                                                                                                                                                                                         Hum.
                                                                                                                                                                                                                                                                       methylenetetrahydrofolate
                                                                                                                                                                                                                                                                                   Rosenblatt D.S., I "Characterization
                                                                                                                                                                                                                                                                                                                 Sibani S., Christensen
                                                                                                                                                                                                                                                                                                                                MEDLINE=20145670;
                                                                                                                                                                                                                                                                                                                                                                                                                        Weisberg I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98387934;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kluijtmans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             van der Put N.M.J., Gabreels F.,
Trijbels F.J.M., Eskes T.K.A.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98213566;
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                                                                                                                                                                                                                                                                                                                                                                                          (MTHFR) associated
                                                                                                                                                                                                                                                                                                                                                                                                        'A second genetic
                                                                                       PATHWAY:
            POLYMORPHISM: VARIANT VAL-222 IS A COMMON POLYMORPHISM WHICH HAS BEEN INPLICATED IN THREE MULTIFACTORIAL DISEASES: OCCUUSIVE VASCULAR DISEASE, NEURAL TUBE DEFECTS (NTD) AND COLON CANCER. DISEASE: DEFECTS IN MTHER ARE THE CAUSE OF HOMOCYSTEINEMIA (HOMOCYSTINURIA II), AN AUTOSOMAL RECESSIVE DISEASE WHICH SHOWS
                                                                                                                                                           SUBSTRATE FOR HOMOCYSTEINE REMETHYLATION TO I CATALYTIC ACTIVITY: 5-METHYLTETRAHYDROFOLATE (CATALYENETETRAHYDROFOLATE + NADPH.
                                                                                                                                                                                                        . Mutat. 15:280-287(2000).
FUNCTION: CATALYZES THE CONVERSION OF 5,10-
METHYLENETETRAHYDROFOLATE TO 5-METHYLTETRAHYDROFOLATE,
                                                                                                                                  ENZYME REGULATION:
                                                                                                                                                  COFACTOR: FAD
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                                                                                                      FOLATE METABOLISM
                                                                                                                                                                                                                                                             Rozen R.;
Rozen R.;
on of six novel mutations in fair reductase (MTHFR)
                                                                                                                                                                                                                                                                                                              PubMed=10679944;
ensen B., O'Ferrall E.,
                                                                                                                                                                                                                                                                                                                                                                         polymorphism in methylenetetrahydrofolate
d with decreased enzyme activity.";
, 64:169-172(1998).
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.J., Milos R., Goyette P.,
ers G.J.H., den Heijer M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9719624;
                                                                                                                                                                                                                                                                                                                                              LEU-572 AND LYS-586.
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                                                                                                                                    ALLOSTERICALLY REGULATED
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SUCH AS DEVELOPMENTAL

DELAY

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SEVERE MENTAL RETARDATION, PERINATAL DEATH, PSYCHIATRIC DISTURBANCES, AND LATER-ONSET NEURODEGENERATIVE DISORDERS. SIMILARITY: BELONGS TO THE METHYLENETETRAHYDROFOLATE REDUCTASE (EC 1.5.1.20/EC 1.7.99.5) FAMILY.

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Matches
       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         EMBL; AF10598
EMBL; AF10598
EMBL; AF10598
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AF105979;
AF105980;
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AF105987; AAD179
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       10.2%; Score 69; DB 28.7%; Pred. No. 14;
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A223439AC8554640 CRC64;
                                                                                      THERMOLABILE; DECREASED ACTIVITY).
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d=VAR_009536.
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Query Match Best Local S Matches 36

ch 10.2%; l Similarity 26.5%; 36; Conservative :

15;

45;

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Gaps

8

Length 1023; Indels

Score 69; DB Pred. No. 24; DS: Mismatches

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RESULT 12
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ID GLT_DROME
AC P33438;
DT 01-FEB-1994
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PROSITE; PS00941; CARBOXYLESTERASE_B_2;
                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-FEB-1994 (Rel.
30-MAY-2000 (Rel.
                                          CARBOHYD
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                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                with sequence similarity tembo J. 9:1219-1227(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olson P.F., Fessler L.I., Nelson R.E., Sterne R.E., Campbell A.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota; Neoptera; Endoptephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
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                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                    FlyBase; FBgn0001114; Glt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Glutactin, a novel Drosophila basement membrane-related glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fessler J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90214632;
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                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: BASEMENT MEMBRÂNES.
-!- PTM: EXTENSIVELY O-GLYCOSYLATED AND ALSO N-GLYCOSYLATED.
-!- PTM: FOUR TYROSINES ARE SULFARED.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE TYPE-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500
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ilidae; Drosophila.
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Last annotation update
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                                                                                                                                                                                                                                                                                                                                                                                               rhabditid nematode species.";
MOL. Biol. Evol. 13:674-684(1996).
-I- FUNCTION: PRECURSOR OF THE EGG-YOLK PROTEINS THAT ARE SOURCES NUTRIENTS DURING EMBRYONIC DEVELOPMENT (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998
15-JUL-1998
15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Rhabditidae; Rhabditinae; Osci_TaxID=57871;
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fam; PF00094; vwd; 1.
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EMBL; EMBL; EMBL;

\$45387; AAB23643.1; -. M59198; AAA32831.1; -. D10850; BAA01623.1; -. X57839; CAA40971.1; -.

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FEBS Lett.
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1: FUNCTION: PLAYS A KEY ROLE IN THE CONTROL OF THE EUKARYOTIC
CELL CYCLE. COMPONENY OF THE KINASE COMPLEX THAT PHOSPHORYLATES
THE REPETITIVE CARBOXYL-TERMINUS OF RNA POLYMERASE II.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=92339744; PubMed=1634002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. COLUMBIA;

MEDLINE=92039027; Pubmed=1937013;

Hirayama T., Imajuku Y., Anai T., Matsui M., Oka A.;

"Identification of two cell-cycle-controlling cdc2 g

Arabidopsis thaliana.";

Gene 105:159-165(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=93005715; PubMed=1840925;
MEPRINE=93005715; PubMed=1840925;
Ferreira P.C.G., Hemerly A.S., Villarroel R., van Montagu M.,
"The Arabidopsis functional homolog of the p34cdc2 protein kir
Plant Cell 3:531-540(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92316202; PubMed-1618302;
Imajuku Y., Hirayama T., Endoh H., Oka A.;
"Exon-intron organization of the Arabidopsis thaliana
genes CDC2a and CDC2b.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
CELL DIVISION CONTROL PROTEIN 2 HOMOLOG A (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                            Inze D., Ferreira P.C.G., Hemerly A.S.,
"Control of cell division in plants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
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                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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InterPro; IPR000719; -.
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P47113;
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DOMAIN 193 201
DOMAIN 265 268
SEQUENCE 574 AA; 66
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Huang M.-E., Chuat J.-C., Galibert F.;
"Analysis of a 42.5 kb DNA sequence of chromosome X reveals three
tRNA genes and 14 new open reading frames including a gene most
probably belonging to the family of ubiquitin-protein ligases.";
Yeast 11:775-781(1995).
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

Transferase; Serine/threonine-protein kinase; ATP-binding;

Transferase; Serine/threonine-protein kinase; ATP-binding;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
01-CCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL 66.1 KDA PROTEIN IN RAD7-HIT1 INTERGENIC REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                 4 PKYKPSSLRTLPETLDPAEYNI ------SPETRRAQ -----AERLAIR ---- 40
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PRFLKKSSSSLPLKISPAQYDIVKHDELLTPGLHRRQRDWNTQQELDSFKEKRSVRHCSN 318
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Search completed: April 29, Job time: 132 sec 2001, 06:47:26

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1: Sp_archea:*
2: Sp_bacteria
3: Sp_fungi:*
4: Sp_human:*
5: Sp_inverteb
6: Sp_manmal:*
7: Sp_mhc:*
8: Sp_organel1
9: Sp_phage:*
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Q9v150 pyrococcus
Q9wxh9 lactobacill
Q9lfz1 arabidopsis
Q9lg30 arabidopsis
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Q9lg30 arabidopsis
Q9lg30 plasmodium
Q9xf46 phaseolus a
Q9xf13 phaseolus v
Q9zb47 streptococc
Q9i8d1 gallus gall
Q9ugr2 homo sapien
Q9ugp8 homo sapien
Q9ugl33 drosophila
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ALIGNMENTS

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NA MEIRGIOV G., MIISHING N.V., MODGILY C., MOILIS	Moshalow C Wilships N W Mohamus C	Tim V Matter D	Tacko b	Kimmel B F	Jalali M	Hostin	Harris N.L.	Glodek A.,	. Fosler C., Gabrielian A.E., Garg N.S., Ge	Durbin	Dodson K., Doup L.E., Downes M., D	de Pabl	Cherry J.M., Cawley S., Dahlke C.,	•	. Borkova D., B	Beeson K.Y., Benos P.	•	Abril J.F., Agbayani	Wan K.H., Doyle C.,	Brandon R.C.,	Sutton G.G., Wortman J.R	George R.A., Lewis S.E.,	. Amanatides P.G., Scherer S.E., Li P.W.,	Adams M.D., Celniker S.E., Holt R.A., Evans	•		RP SEQUENCE FROM N.A.		NCBI_TaxID=7227;	Ephydroidea; Drosophi	Pterygota; Neoptera; Endopterygota; Diptera	Eukarvota: Metazoa: Arthropoda: Tracheata:		GN CG12859 FROIEIN:	01-MAY-2	01-MAY-2000 (TrEMBLrel. 13, Last	01-MAY-2000 (TrEMBLrel. 13, Crea	Q9V753;	ID Q9V753 PRELIMINARY; PRT; 113 AA.	RESULT 1 Q9V753
IS O., MOSILLELL A.,	, , ,	7 :		Lai Z	nnison J.A. Ketchum K.A.	1. H., Ibeqwam C.,	lez J.R., Houck J.,		×.		S., Dunkov B.C., Dunn P.,	Lz S.M.,	L.B., Davies P.,	E., Center A., Chandra I.,	Brottier P	Во	roglu L., Beasley E.M.,	Pfannkoch C., Baldwin D.,	Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,	Champe M., Pfeiffer B.D.,	ing Q., Chen L.X.,	Richards S., Ashburner M., Henderson S.N.,	.A., Galle R	C.A., Gocayne J.D.,					•		Brachycera; Muscomorpha;	Hexapoda: Insecta:			update)	odate)				

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"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
Science 287:2185-2195(2001).
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01-OCT-2000 (TrEMBLrel.
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SEQUENCE 113 AA; 13134 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL; aF221695; aAF36389.1; -.
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Last annotation update)
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Best Local :
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
(Chen F., Liu K.C., Epstein J.A.,
"Lbx2, a novel murine homeobox g
"Lbx2, a **ressed in the develo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9KI98;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 37.1 KDA PROTEIN.
                                                                                                                                                     PFAM; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
PROSITE; PS50071; HOMEOBOX_2; 1.
HOMEOBOX; DNA-binding; Nuclear protein.
SEQUENCE 195 AA; 20916 MW; E106CE108933DE45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Multiple gene products and sequences required f mobilizable integrated Bacteroides element NBU1.
J. Bacteriol. 182:928-936(2000).
EMBL; AF238807; AAF74439.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=20115534; PubMed=10648516;
Shoemaker N.B., Wang G.R., Salvers A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteroides uniformis.
Bacteria; CFB group; Bacteroidaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9KT98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LADYBIRD-LIKE HOMEODOMAIN PROTEIN LBX2 LBX2H OR LBX2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9WUN8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9WUN8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein. SEQUENCE 313 AA; 37128 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1342288;
                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO; IPRO00047; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 AMLAWLY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 ALLRWAY 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 PKYKEAARKRIGDDRNP-DFE-----ELENVLLQSDLAEKIVNEFHTPNKRSIV--P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 PKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLKREYLLQYNDPNRRGLIENP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dev. 0:0-0(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P23441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF146150; AAD31905.1;
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15; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1FTT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lbx2h.
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        10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the developing
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        Score 74;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74.5; DI
Pred. No. 6.9;
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D1D43577FDB882D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene related to the Drosophila ladybird loping urogenital system, eye, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195
            DB 11;
4.4;
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                                        Length 195
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Murinae; Mus
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Best Local
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
TRYPTOPHAN SYNTHASE, SUBUNIT BETA (TRPB-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ248284; CAB49501.1; -.
HSSP; P00933; 2WSY.
             Senba M., Nakashima Y., Miake F., Watanabe K.; "Cloning and Exression of the beta- N-Acetylglucosaminidase Gene Lactobacillus casei ATCC 27092 and Characteristics of the enzyme expressed in Escherichia coli."; Submitted (WAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
BETA N-ACETYLGLUCOSAMINIDASE.
                                                                                         SEQUENCE FROM N.A. STRAIN-ATCC 27092;
                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota;
NCBI_TaxID=29292;
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 SEQUENCE
                                                                                                                                                                                                                                     Q9WXH9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heilig R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ORSAY;
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                                                                                                                                                                     Lactobacillus casei
                                                                                                                               NCBI_TaxID=1582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yrococcus abyssi
                                                                                                                                                                                                                                                                                                                                           62
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                                                                                                                                                                                                                                                                                                                                                                                          LRTLPETLDPAEYNISPET-----RRAQAERLAIRAQLKREYLLQYNDPNRRGLIE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLRTLPETLDPAEYNISPE-----TRRAQAERLAIRAQ----LKREYLLQ-YNDPNR 56
                                                                                                                                                                                                                                                                                                                 IPGELRKLYSKIGRPTPLFRATNLEKLLG 102
                                                                                                                                                                                                                                                                                                                                                                   LPDLPEPLDPP----LDPETEEPIDIEKLKRIFAEEL-VKQEISRE----RY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RDGL---AARLGLANAQVVTWFQNRRAKLKRDVEEMRADVASLCGLSPGVLCY 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R-GLIENPALLRWAYARTINVYPNFRPTPKNSL-----MGALCGFGPLIFIY 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPRATPQ----PSEGRAAPEAPPGPGAGVRRRRKSRTAFTAQQVLELERRFVFQKYLAPSE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
 526 AA;
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                                                                                                                                                                                                                                                 PRELIMINARY;
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  56835 MW;
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Pred.
  255D541FA300C723 CRC64;
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No.
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                                                                                                                                                      group; Lactobacillaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 451;
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                                                                                                                                                                                                                                                                                                                                                                   IE 73
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT
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Best Local S
Matches 27
          Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mutharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                             Ecker J.R.
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L. Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee Lenz C., Li J., Liu A., Liu S., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                      Shinn P.P., Buehler E.E., Dunn P.P., Feng J.J., Kim C.C., Li Y.Y. Walker M.M., Altafi H.H., Araujo R.R., Conn L.L., Conway A.A.B., Gonzalez A.A., Hansen N.N.F., Huizar L.L., Kremenetskaia I.I., Lenz C.C., Li J.J., Liu S.S., Luros S.S., Rowley D.D., Schwartz Toriumi M.M., Vysotskaia V.V., Yu G.G., Davis R.R.W., Federspiel N.N.A., Theologis A.A., Ecker J.J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids Brassicales; Brassicaceae; Arabidopsis.
SEQUENCE
                                                                                                                                                                  Submitted (MAY-2000)
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27; Conser
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nilarity 30.0%;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
3945B20167DCC56B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142
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Kremenetskaia I.I.,
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e; eurosids II;
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Matches '28; Conserv
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Best Local S
Matches 28
                                                                                                                                                         Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafl H., Bel B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaverl A., Torlumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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F14J16.7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2000)
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28; Conserv
     Conservative
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 15, Last annotation update)
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                                                                                                                                67645 MW; CAA6BD39DF018084 CRC64;
10.4%; Score 70.5; I
26.9%; Pred. No. 39;
Live 18; Mismatches
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26.9%; Pred. No. 33;
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39;
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19;
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Gaps
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RESULT 10
Q9NPH8
ID Q9NPH8
AC Q9NPH8
DT 01-OCT
DT 01-OCT
DT 01-OCT
DE SOX18
GN SOX18
GN SOX18
OC Eukary
OC Mammal
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RP SEQUEN
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Best Local Similarity
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01-OCT-2000
01-OCT-2000
                                     Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
 SEQUENCE FROM N.A.
                      NCBI_TaxID=9606;
                                                                                          SOX18 PROTEIN.
                                                                                                                                             Q9NPH8;
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Q9U3U8;
01-MAY-2000 (TremBLrel.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Delbac Fr., Soldati D.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF222717; AAF25689.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00063; myosin_head; PFAM; PF00400; WD40; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determinant of Plasma Membra Submitted (JAN-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum.
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2000 (TrEMBLrel. 15, MYOSIN PFM-C (FRAGMENT).
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PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO; IPR001680; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
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                                                                                                                                                                                                                                                                         101 KYVMKFLACAGSDIKKRSLIESQVLESNPLLEAFGNARTLRNNNSSRFGKYIELQFSVDH 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPR001609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO;
                                                                                                                                                                                                                          161 KNYIKGKLCGAKILTYLL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           530
                                                                                                                                                                                                                                             85 KNSLMGALCGFGPLIFIYYIIKTERDRKEKLIQEGKLDRTFHLSY
                                                                                                                                                                                                                                                                                                      46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                  EYLLQY-----NDPNRRGLIE-----NPALLRWAYARTIN-------VYPNFRPTP 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIFEQISEKILM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNFRPTPKNSLMGALCGFGPLIFIYYIIKTERDRKEKLIQEGKL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDTDIQRISGETRELQLEKNSIQERLHRSYAV-VDEMVTREVKKDPA-VRQVYKLLTSIH 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P08799; 1MND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000169;
                                                                                                    O (TrEMBLrel. 15,
O (TrEMBLrel. 15,
O (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                              2067 AA;
                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herm A.,
                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                          10.4%;
                                                                                                                                                                                                                                                                                                                                                                                            239980 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Geiter A., Frank B., Schwarz E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Membrane Localization
                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                               Created)
                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                        Score 70.5;
Pred. No. 1
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                                     Craniata; Ve Catarrhini;
                                                                                                                                                          PRT;
                                                                                                                                                                                                                      -EKVRVCDQQEGERNYHIFY 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              80B5F9077EDED3D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDRERRETVDYEKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2067
                                                                                                                                                        384
                                                 Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                        ₽Α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AΑ
                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                     Length 2067;
                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soldati T.,
                                                                                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Essential
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OCTOR REPORT OF THE REPORT OF 
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Query Match
Best Local Similarity
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Best Local :
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Q25693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                          Exp. Parasitol. 79:137-147(1994).
EMBL; U04640; AAA21513.1; -.
HSSP; P13569; INBD.
                                                                                                                                                                                                                                                                                       Rubio J.P., Cowman A.F.;
"Plasmodium falciparum: the pfmdr2 protein is
chloroquine-resistant isolates of the malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2000 (Tr
PFMDR2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription factor.";
Gene 161:223-225(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochim. Biophys.
                                                                                  PROSITE; PS00211; ABC_TRANSPORTER; ATP-binding; Transport. SEQUENCE 1025 AA; 119152 MW; 9:
                                                                                                                                                                                                                                                                                                                                                                                STRAIN-D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Muscat G.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "cDNA cloning, tissue expression
homolog of SOX18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=BRAIN;
                                                                                                                                                 PFAM; PF00005; ABC_tran; 1. PFAM; PF00664; ABC_membrane;
                                                                                                                                                                                      INTERPRO; IPR001140; -.
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94333528; PubMed=7914495;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence and expression of sox-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn T.L., Mynett-Johnson L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stanojcic S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            lasmodium falciparum.
ukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 PKYKPSSLRTLPETLDPAEYNISPETR--RAQAERLAIR-----AQLKREYLLQYN 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGFGPLIFIYYIIKTERDRKEKLIQEGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDLHNAVLSKMLGKAWKELNAAEKRPFVEEAERLRVQHLRD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ243896; CAB95835.1; -. AB033888; BAA94874.1; -. NCE 384 AA; 40891 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OCT-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOX18 gene:
iophys. Acta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stevanovic M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKKQARKARRLEPGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yoshikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
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    10
33
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apicomplexa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PNRRGLIENPALLRWAYARTINVYPNFRPTPKNSLMGAL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA cloning and high resolution mapping."; 1492:237-241(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wright E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327462E519770062 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Masuho Y., Mura
and chromosome
                                                                                    91AF3BD8916D520D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
  70;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding a new HMG-box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1025
    96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
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                     5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muramatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
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                                                                                                                                                                                                                                                                                           not overexpressed
parasite.";
                     Length 1025;
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RESULT
Q9XF13
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Q9XF46
DR RT 
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Best Local Similarity 34.v
"""hes 16; Conservative
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                          Submitted (FEB-1999) to the EMBL EMBL; AF126737; AAD30494.1; --
INTERPRO; IPR000719; --
INTERPRO; IPR001245. --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9XF46;
Q9XF46;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              Q9XF13 PRELIMINARY; PRT; 280 AA.
Q9XF13;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CELL DIVISION CONTROL PROTELN 2 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U1-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) CELL DIVISION CONTROL PROTEIN 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adventitious root in mung bean.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Luo S., Liu S.-L.,
"Cdc2 gene cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phaseolus aureus (Mung bean) (Vigna radiata).
Eukaryota: Viridiplantae: Embryophyta: Trache
                                                                                                                                                                               SEQUENCE FROM N.A.
Luo S., Liu S.-L.,
                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
                                                                                                                                                                                                                                                                                                                          Phaseolus vulgaris (Kidney bean) (French bean)
Eukaryota; Viridiplantae; Embryophyta; Tracheop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00108; PROSITE; PS50011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00069; pkinase; 1. PRINTS; PR00109; TYRKINASE
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                                                                                                                                                                                                                                                                           Fabales; Fabaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   division.
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                                                                                                                                          wang Y., Wang Y.-C.
and its expression
in mungbean.":
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32166 MW;
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Pred. No. 20;
12; Mismatches
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SEQUENCE

280 AA;

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Matches 27; Conserv
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29ZB47;
01-MAY-1999
01-MAY-1999
Kendrick-Jones :
Submitted (JUN-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pyogenes.
Bacteria; Firmicutes; B.
Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Podbielski A., Woischnik M., Leonard B.A.B., "Characterization of nra, a global negative 1 streptococci."; Mol. Microbiol. 31:0-0(1999).
EMBL; U49397; AAC97148.1; -. SEQUENCE 742 AA; 83682 MW; 97AlfF44B4ECB5
                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
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                                                                         SEQUENCE FROM N.A.
                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                            MYOSIN VI.
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Pred. No. 65;
17; Mismatches
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Best Local Similarity
Matches 33; Conserv
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J. Cell Biol. 143:1535-1545(1998).
EMBL; AJ278608; CAB96536.1;
SEQUENCE 1276 AA; 147603 MW; 5F6AEE43A6FB260F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Buss F., Kendrick-Jones J., Lionne C., Knight A.E.,
                                                                                                                                                                                                                                                                                                                                                                                          Luzio P.
                                                                                                                                  114
                                                                 170
                                                                                                                                                                  5 KYKPSSLRTLPETLDPAEYNISPETRR-----AQAERLAIRAQL------KREYLLQY--
                                                                                                                                  KYQGRSLGTLP----PHVFATADKAYRDMKVLKMSQSIIVSGESGAGKTENTKFVLRYLT 169
                                                                                            ----NDPNRRGLIENPALLRWAYARTI-----NVYPNERPTPKNSLMGALCGEGP 97
                            LIFIYYIIKTERDRKEKLIQEGKLDRTFHLSY 129
                                                                ESYGTGQDIDDRIVEANPLLEAFGNAKTIRNNNSSRFGKFVEIHFNEKNSVVG----GF--
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KSRICVQGKEERNYHIFY 249
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    69.5
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503
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length: 2000000000
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Match
    100.0
74.2
111.2
10.6
10.3
10.3
10.2
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10.2
10.2
                                                                                                                                                                                                                                                                                                                              is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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678
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Copyright (c) 1993 - 2000 Comp
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                                                                                                                                                                                                                                       ID
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R88358
R88359
                                                                                                                  B53504
G33365
B35797
                                                                                                                                                                           W69225
Y76629
                      Y96186
G54044
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363.612 Million cell updates/sec
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Human methylene-te
Human methylenetet
Arabidopsis thalia
Arabidopsis thalia
                                                                                                                                                                                                                                   Description
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Zea mays protein f
Protein involved i
                                                                                                                                                                       NADH dehydrogenase
Human ovarian tumo
                                                                            Human methylene-te
                                                                                              Oryza sativa Cdc2
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4.5	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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6759	47	G39985	G39986	G14733	G56114	G14734	G54995	Y78833	Y77281	Y75537	Y21591	R67590	G33356	G33357	G33358	G59502	в42915	Y29975	Y76168	B25784	R15223	Y28426	G47999	Y75683	W76439	Y03636	Y29193	Y73366	Y02827	G11213	54 C	11	G54043
Hepatitis C virus	is thal	Arabidopsis thalia	CO	eguen	Streptomyces coeli		Human secreted pro	Hepatitis C virus	Zea mays protein f	Zea mays protein f	Zea mays protein f	Arabidopsis thalia	Human ORFX ORF2679	Human electron tra	Human secreted pro	Human secreted pro	OV-16 antigen. On	an bra	Arabidopsis thalia	meningi	Human p53 regulate	9		ne 2	O.f.	S	Arabidopsis thalia	is thal	Arabidopsis thalia				

ALIGNMENTS

ΧPD XX × 20 × XXX RESULT NADH dehydrogenase subunit; sympathetic nervous system disease; myopathy; nicotinamide-adenine dinucleotide dehydrogenase; cancer; leukaemia; immune system disorder; neurodegenerative disease; therapy; NDS-2. W69225; W69225 standard; Protein; 129 17-JAN-1997; 17-DEC-1997; 23-JUL-1998 WO9831815-A2 Homo sapiens. NADH dehydrogenase subunit NDS-2. 18-FEB-1999 (INCY-) INCYTE PHARM INC. (first entry) 97US-0785065 97WO-US23970 ĄΑ

Human nicotinamide-adenine di:nucleotide dehydrogenase sub:units - useful for, e.g. diagnosis, treatment and prevention of cancer, myopathy, immune system disease and neuro:degeneration

WPI; 1998-414112/35. N-PSDB; V44787. Bandman O,

Goli SK,

Hillman JL;

Claim 19;

Fig 2; 80pp; English.

Cells

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Y7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the NADH (reduced nicotinamide-adenine dinucleotide) dehydrogenase subunit, NDS-2, of the invention. Cell containing the DNA are used to produce the recombinant subunits. Antagonists of NDS-1 (typically antisense sequences or ribozymes) used to treat or prevent cancer (leukaemia and solid cancers) and
                      Rosenthal A,
                                                                                                                  09-APR-1998;
                                                                   (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                 09-APR-1998;
                                                                                                                                                                                                                21-OCT-1999
                                                                                                                                                                                                                                                               DE19817557-A1
                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence tag; EST; human; ovarian tumor; anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                              Human ovarian tumor EST fragment encoded protein 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y76629;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                   Specht T, Hinzmann B,
                                                                                                                                                                                                                                                                                                                                                             treatment
                                                                                                               98DE-1017557
                                                                                                                                                                 98DE-1017557.
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                   Schmitt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                   Pilarsky
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                   Dahl
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RESULT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes novel nucleic acid (cDNA) sequences (A) which have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (1) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of ovarian cancer; (ii) directly for treating this form of cancer (including ovarian cancer; (ii) directly for treating this form of cancer (including ovarian cancer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different
                                                                                                                                                                                                                                                                 Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrolntestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. Y76505-Y76638 represent protein fragments encoded by the human overian tumor cDNA library derived EST fragments represented in Z77450-Z77572.
                                                                                                                                                                                                                                                                                                                                                                     Human colon cancer antigen protein sequence SEQ ID NO:1044
                                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         B53504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B53504 standard; Protein; 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid sequences expressed in ovarian, and some other, cancer tissues, and derived polypeptides, for treatment of ovarian cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-591920/51
                                      08-MAR-2000;
                                                                                                                        WO200055351-A1
                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                         infectious disease; cardiovascular
                                                                                                                                                                                                                                                neural disorder; immune system disorder; muscular disorder;
12-MAR-1999;
                                                                                                                                                                                                                        reproductive disorder; gastrointestinal disorder; renal disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 GFGPLIFIYYIIKTERDRKEKLIQEGKLDRTFHLSY
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                        2000WO-US05883
99US-0124270.
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(HUMA-) HUMAN GENOME SCI INC

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RESULT
G33365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 15;
25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

19-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer \,\cdot\,
                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                                                   18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                    G33365 standard; Protein; 290 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11;
                                                                                                                                                                                                        EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen
                                                                                                                                                       25-FEB-2000;
                                                                                                                                                                                                                                Zea mays subsp. mays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                114 KLIQEGKLDRTFHLSY 129
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                                                                                                                                                                                                                                                                                                         mays protein fragment SEQ ID NO: 40416
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DB; C98261.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 1624; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 AA;
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                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                       2000EP-0301439
99US-0121825.
99US-012548.
99US-0125788.
99US-0125787.
99US-0126765.
99US-0127462.
99US-0128234.
99US-0128234.
99US-0128834.
99US-0128874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.2%;
93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 76; DB 21;
Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 16;
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23-JUN 1999
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01-JUL 1999
01-JUL 1999
02-JUL 1999
02-JUL 1999
03-JUL 1999
04-JUL 1999
05-JUL 1999
06-JUL 1999
07-JUL 1999
08-JUL 1999
08-JUL 1999
08-JUL 1999
11-JUL 1999
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07-JUN-1999;
08-JUN-1999;
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22-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
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01-JUN-1999
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07-MAY-1999
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05-MAY-1999
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23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-1999
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       9908-013847
9908-0139452
9908-0139453
9908-0139455
9908-0139456
9908-0139460
9908-0139461
9908-0139461
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9908-014334
9908-014332
9908-0144333
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99US-0137502
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99US-0138540
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99US-0137222
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99US-0136392
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99US-0134941
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99US-0132407
 99US-0144335
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20-JUL-1999; 20-JUL-1999; 20-JUL-1999;

99US-0144352. 99US-0144632. 99US-0144884. 99US-0144814.

22-JUL-1999; 22-JUL-1999;

99US-0145087

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RESULT
B35797
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Best Local S
Matches 32
Nucleic acids useful for producing transgenic plants, preferably maize,
                       WPI; 2000-687333/67.
N-PSDB; C83104.
                                                                                                                                                                   Cell cycle regulation; corn; transgenic plant; cyclin; maize; soybean; cyclin-dependent kinase; sunflower; sorghum; canola; wheat; alfalfa; cotton; rice; barley; millet.
                                                Helentjaris TG,
                                                                                                  13-APR-2000; 2000WO-US09975
                                                                                                                                                                                                      Protein involved in cell cycle regulation SEQ ID 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                              26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                 (PION-) PIONEER HI-BRED INT INC.
                                                                                  22-APR-1999;
                                                                                                                     02-NOV-2000.
                                                                                                                                      WO200065040-A2
                                                                                                                                                       Zea mays
                                                                                                                                                                                                                                             в35797;
                                                                                                                                                                                                                                                           B35797 standard; Protein; 292
                                                                                                                                                                                                                          23-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-1999;
26-OCT-1999;
                                                                                                                                                                                                                                                                                                         123 if1 125
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                                                                                                                                                                                                                                                                                                                                     99 IFI 101
                                                                                                                                                                                                                                                                                                                                                                      10 plfcpgplvarp----pa--sssppagrpasqtlarrarekldamfgyrkadpdleaggs 63
                                                                                                                                                                                                                                                                                                                                                                               4 PKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLKREYLLQYN--DPNRR----
                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                  99US-0130849
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990S-0161404.
990S-0161405.
990S-0161406.
990S-0161360.
990S-0161361.
990S-0161361.
990S-0161361.
990S-0161392.
990S-0161992.
990S-0161992.
990S-0161992.
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99US-0160768.
99US-0160770.
                                                Habben
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99US-0160815
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99US-0160741.
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9908-0159637
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                                                JΕ,
                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                               Sun
                                                                                                                                                                                                                                                                                                                                                                                                        Score 72; DB 21;
Pred. No. 1.9;
5; Mismatches 44
                                               Y,
                                                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                         32;
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18-AUG

99US-0149368 99US-0149175 99US-0149722 99US-0149722 99US-0149723 99US-0149929 99US-0149929 99US-0149930 99US-0149936 27-JUL-1999 28-JUL-1999 02-AUG-1999 02-AUG-1999 2-AUG-1999 03-AUG-1999 04-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 06-AUG-1999

> 99US-0145276. 99US-0145913. 99US-0145918. 99US-0145919.

99US-0145386 99US-0146386 99US-0146388 99US-0147038 99US-0147203 99US-0147302 99US-0147302 99US-0147303 99US-0147303 99US-0147303 99US-0147416 99US-0147935 99US-0147935 99US-0147935 99US-0147935 99US-0148319 99US-0148319 99US-0148319 99US-0148319 99US-0148319

01-SEP-1999; 07-SEP-1999; 10-SEP-1999;

99US-0150884 99US-0151066 99US-0151080 99US-0151080 99US-0151303 99US-0151333 99US-015133 99US-0153375 99US-0153758 99US-0153758

13-SEP-1999; 15-SEP-1999; 16-SEP-1999;

99US-0154779. 99US-0154779.

04-OCT-1999 05-OCT-1999

99US-0156458 99US-0156596 99US-0157717 99US-0157753 99US-0158029 99US-0158029 99US-0158023 99US-0158232 99US-0158232 99US-0159294 99US-0159294 99US-0159294 99US-0159330

13-OCT-1999

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RESULT
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ID W95690
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XX W9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC and cyclin-dependent kinases. The DNA sequences are also useful as probes CC for detecting deficiencies in the level of mRNA in screening for desired CC transgenic plants, for detecting mutations in the gene, for monitoring CC upregulation of expression or changes in enzyme activity in screening CC assays of compounds, for detecting any number of allelic variants, CC orthologs or paralogs of the gene, and site-directed mutagenesis in CC eukaryotic cells. The DNA sequences are also useful for recombinant CC expression of the encoded polypeptides and as immunogens for preparing CC enzyme agonists and antagonists, and as immunogens or antigens to obtain CC entibodies. The antibodies are useful in assaying expression levels of CC entibodies. The antibodies are useful in assaying expression levels of CC entibodies. The antibodies are useful in assaying expression levels of CC entibodies. The antibodies are useful in assaying expression levels of CC cell cycle regulatory protesins, for identifying and isolating nucleic CC acids from expression libraries, for identifying homologues of CC coll cycle regulatory protesins, for identifying homologues of the proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cycle polynucleotides. The cell cycle polynucleotide sequences are useful for producing transgenic plants such as maize, soybean, sunflower sorghum, canola, wheat, alfalfa, cotton, rice, barley and millet with increased levels of cell cycle gene activity, such as activity of cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide sequences C83101 - C83113 encode proteins B35794 - B35806 which are involved in regulating the cell cycle. The protein and DNA sequences have been isolated from Zea mays (corn), and the invention also includes oligonucleotides C83114 - C83139 which are related to the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cdc2; protein kinase; diagnosis; infection; immunosuppression;
AIDS; acquired immunodefiency syndrome; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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New isolated polynucleotide encoding a Pneumocystis carinii Cdc2 polypeptide - useful for diagnosing or monitoring P. carinii
                                                                                                          WPI; 1999-080877/07.
                                                                                                                                                                                                                                              (MAYO-) MAYO
                                                                                                                                                                                                                                                                                                                  13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                     12-JUN-1998;
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239 tfpkwppvdlatvvptlepsgidllskmlrldpskritaraalehdy 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cdc2 protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                  FOUNDATION
                                                                                                                                                                          Leof
                                                                                                                                                                                                                                                                                                                  97US-0874347
                                                                                                                                                                                                                                                                                                                                                                                     98WO-US12100
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                                                                                                                                                                          Limper AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                              Thomas CF
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PT PT XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AIDS), solid tumors, hematological malignancies, organ transplantation, and inflammatory conditions. The polypeptides are additionally useful in identifying agents that inhibit the phosphorylation activity of p. carinii Cdc2 polypeptides. The polypeptide and its antibodies are useful for diagnosing or monitoring P. carinii infection in patients. The P. carinii Cdc2 polypeptides allow a therapeutic approach to treating P. carinii pneumonia because they are not limited by significant side effects. Polynucleotides encoding P. carinii Cdc2 enable in vitro
                                                                                                                  Human methylene:tetra:hydro:folate reductase cDNA probe - for detection of sequence abnormalities in methylene:tetra:hydro:folate reductase e.g. in cardiovascular, neurological or folic acid
                                                                                                                                                                                   WPI; 19
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methylene-tetrahydrofolate-reductase; MTHFR; gene therapy; cardiovascular disease; neurological disease; folic acid metabolism; EC-1.5.1.20; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           production of the protein, which can be used in studying (especially its life cycle) and developing new therapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumonia in patients with chronic immunosuppresion. Conditions associated with P. carinii include acquired immune deficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a Cdc2 polypeptide The Cdc2 polypeptides are useful in treating
                                                                        Disclosure;
                                                                                                       metabolism
                                                                                                                                                                                                                                Goyette P,
                                                                                                                                                                                                                                                                                             26-MAY-1994;
                                                                                                                                                                                                                                                                                                                          25-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                         07-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human methylene-tetrahydrofolate-reductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R88358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R88358 standard; Protein; 656 AA
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                                                                                                                                                                                                                                                             (UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 afpkwqaqdlativptldpagldllskmlryepnkritarqalehey 286
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                                                                                                                                                                                   1996-030565/03.
DB; T09689.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pages 44-45; 67pp; English
                                                                                                       disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 AA;
                                                                                                                                                                                                                              Rozen R;
                                                                      Fig.6A-6C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                           94GB-0010620
                                                                                                                                                                                                                                                                                                                          95WO-CA00314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%;
                                                                      66pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 69.5; D
Pred. No. 3.9;
                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in treating P. carinii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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1;

This is the protein sequence encoding human MTHFR, the gene of which has been localised to chromosome 1p53. Deficiencies of this protein may lead to cardiovascular and neurological disorders and disorders influences by folic acid metabolism.

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                                                                                                             Query Match
Best Local Similarity
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Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                        The gene encoding this human MTHFR protein has been localised chromosome 1p36.3. Deficiencies of this protein may lead to cardiovascular and neurological disorders and disorders influe by folic acid metabolism.
                                                                                                                                                                                                                                                                                  uman methylene:tetra:hydro:folate reductase cDNA probe - for detection of sequence abnormalities in methylene:tetra:hydro:folate reductase e.g. in cardiovascular, neurological or folic acid metabolism disorders
                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                        Disclosure; Fig.1A-1F; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                            N-PSDB; T09694.
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-030565/03.
                                                                                                                                                                                                                                                                                                                                                                                                  Goyette P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-DEC-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09533054-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methylene-tetrahydrofolate-reductase; MTHFR; gene therapy; cardiovascular disease; neurological disease; folic acid metabolism; EC-1.5.1.20; enzyme.
                                          462 eplaaetsllkeellrv---nrggil---
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human methylene-tetrahydrofolate-reductase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                         (UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-1995
95 FGP---LIF--IYYIIKTERDRKEKLIQ---EGKLDRTFHL 127 :|| :| :| :| :|
                                                   35 ERLAIRAQLKREYLLQYNDPNRRGLIENPALLRWAYARTINVYDNFRPTPKNSLMGALCG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R88359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88359 standard; Protein; 660 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 500 wgpsggyvfqkaylefftsretaeallqvlkkyelrvnyhl 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 FGP---LIF--IYYIIKTERDRKEKLIQ---EGKLDRTFHL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 ERLAIRAQLKREYLLQYNDPNRRGLIENPALLRWAYARTINVYPNERPTPKNSLMGALCG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                                                                                                                                                   660 AA;
                                                                                                                                                                                                                                                                                                                                                                                               Rozen R;
                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 656
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                                                                                                         10.2%; Score 69; DB 17; 28.7%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.2%;
                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                      ----tinsqpningkpssd---pivg 503
                                                                                             32;
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                                                                                                                      Length 660;
                                                                                             Indels
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                                                                                         Gaps
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DЪ Qy DЬ Qy

95

504 wgpsggyvfqkaylefftsretaeallqvlkkyelrvnyhl 544

FGP---LIF--IYYIIKTERDRKEKLIQ---EGKLDRTFHL 127

ERLAIRAQLKREYLLQYNDPNRRGLIENPALLRWAYARTINVYDNFRPTPKNSLMGALCG

----tinsqpningkpssd---pivg 503

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Y96186
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                         Query Match
Best Local 9
            Matches
                                                                                                                                                                                                                        The present sequence is that of human methylenetetrahydrofolate reductase (MTHFR), an enzyme catalysing the NADPH-linked reduction of 5,10-methylenetetrahydrofolate to 5-methyletrahydrofolate, a co-substrate for methylation of homocysteine to methionine. A cDNA probe for human MTHFR is claimed. This probe can be used to identify MTHFR sequence abnormalities in individuals with severe or mild MTHFR deficiency. MTHFR deficiency my be associated with a cardiovascular disorder, cancer (especially neuroblastoma or colorectal carcinoma), osteoporosis, neural tube defect in an
                                                                                              Sequence
                                                                                                                      treating MTHFR deficiency by gene therapy or by administration of MTHFR protein. Cancer can be treated by inhibiting MTHFR gene expression or MTHFR protein activity, or by administering an agent that modifies MTHFR gene expression.
                                                                                                                                                                                         colorectal carcinoma), osteoporosis, neural tube defect in an offspring of a patient, neurological disorders, and other disorders influenced by folic acid metabolism. Also claimed are methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA probe for the human methylenetetrahydrofolate reductase (MTHFR), useful in gene therapy and for diagnosing or treating MTHFR deficienc which is associated with cardiovascular disorders or cancer
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1A-F; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; A50633, A50634.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methylenetetrahydrofolate reductase; MTHFR; human; folic acid; cardiovascular disorder; cancer; neuroblastoma; colorectal carcinoma; osteoporosis; neural tube defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYMC-) UNIV MCGILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological disorder; gene therapy; diagnosis
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           . Similarity
29; Conserv
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                                                                                                  660
         Conservative
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                                                                                                AA;
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                        10.2%; Score 69; DB 28.7%; Pred. No. 13;
         14;
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     Mismatches
                                          DВ
                                      21;
       32;
                                      Length 660;
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   Indels
   26;
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Gaps
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RESULT
G54044
ID G5
XX
AC G5
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   PXPX
03-JUN-1999

04-JUN-1999

07-JUN-1999

08-JUN-1999

10-JUN-1999

110-JUN-1999

14-JUN-1999

16-JUN-1999

17-JUN-1999

18-JUN-1999

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18-JUN-1999
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25-MAY-1999;
27-MAY-1999;
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4-MAY-1999;
19-MAY-1999;
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29-MAR-1999;
01-APR-1999;
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01-JUN-1999
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20-MAY-1999
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23-MAR-1999
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990S-0123E83
990S-0125788
990S-0125788
990S-0126785
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12-AUG-1999;
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13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
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09-JUL-1999
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27-JUL-1999
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13-JUL-1999
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18-JUN-1999
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1-JUL-1999;
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99US-0147192

99US-0147260

99US-0147416

99US-0147416

99US-0147935

99US-0148171

99US-0148341

99US-0148361

99US-0148565

99US-014968

99US-0149722

99US-0149722
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990S-0145145
990S-0145145
990S-0145218
990S-0145224
990S-0145913
990S-0145913
990S-0145913
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99US-0145089.
99US-0145192.
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99US-0145088
99US-0145085
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99US-0144884.
99US-0144814.
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99US-0144332.
99US-0144333.
99US-0144334.
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99US-0142920.
99US-0142977.
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99US-0141287.
99US-0141842.
99US-0142154.
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99US-0147302.
99US-0147192.
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99US-0142390
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99US-0144352
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99US-0140823
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5-0146386
5-0146388
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3-0147038
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-0140353.
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RESULT 11
G11215
ID G11215
XX
AC G11215
XX
PDT 17-OCT
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Best Local s
Matches 17
                  17-oct-2000
                                                                      G11215 standard;
                                                  G11215;
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$-OCT-1999

26-OCT-1999

26-OCT-1999

26-OCT-1999

28-OCT-1999

28-OCT-1999

28-OCT-1999

29-OCT-1999
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29 - SEP - 1999

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13 - OCT - 1999

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14 - OCT - 1999
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18-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
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23-SEP-1999;
                                                                                                                                                                       N
                                                                                                                                 ch 10.1%;
l Similarity 36.2%;
17; Conservative
                  (first entry)
                                                                                                                                                                                                                                               99US-0160989
99US-0161404
99US-0161405
99US-0161369
99US-0161360
99US-0161360
99US-0161361
99US-0161920
99US-0161922
99US-0161932
99US-0161932
99US-0161932
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99US-0151065
99US-0151066
99US-0151080
99US-0151438
99US-0151438
99US-0151439
99US-0154038
99US-0155463
99US-0155465
99US-0155465
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99US-015753
99US-015823
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99US-0149902.
99US-0149930.
99US-0150566.
                                                                      Protein;
                                                                       237
                                                                                                                                                                                          Score 68.5; DB Pred. No. 3.2; 8; Mismatches
                                                                                                                                                                                             8;
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                                                                                                                                                                                                                       В
                                                                                                                                                                                          21;
                                                                                                                                                                                                                  Length
                                                                                                                                                                                         Indels
                                                                                                                                                                                                                  204;
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                                                                                                                                                                                    Gaps
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       24 - MAX - 1999

25 - MAX - 1999

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20 - JUN - 1999

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05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
06-MAY-1999;
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21-MAY-1999;
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09-MAR-1999;
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99US-0130510
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99US-0132487
99US-0134477
99US-013425
99US-013425
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99US-0134768
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99US-013522
99US-0134768
99US-013522
99US-013622
99US-0139452
99US-0139453
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99US-0139453
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99US-0123180.
99US-0123548.
99US-0125788.
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21-JUN-1999; 22-JUN-1999; 23-JUN-1999;

-01

S-0140991 S-0141287 S-0141842

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RESULT 12
G54043
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В
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Matches 17
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25-OCT 1999;
26-OCT 1999;
26-OCT 1999;
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22-OCT-1999;
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14-OCT-1999;
14-OCT-1999;
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                                                Arabidopsis
                                                                                       G54043
                                                                                                          G54043 standard; Protein; 237 AA.
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07-OCT-1999
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05-OCT-1999
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                                                                                                                                                          2 SFPKYKPSSLRTLPETLDPAEYN-ISPETRRAQAERLAIRAQLKREY 47 :|||:||:|| || || : :| :|: || ||: || 183 afpkwkptdletfvpnldpdgvdllskmllmdptkrinaraalehey 229
                                                                                                                                                                                                     17; Conservative
                                                thaliana
                                                                   (first entry)
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99US-0153758.
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99US-0151438.
99US-0151930.
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                                                protein fragment SEQ ID NO:
                                                                                                                                                                                                     8;
                                                                                                                                                                                                    Score 68.5; D. Pred. No. 3.9; B; Mismatches
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23-JUL-1999

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13-AUG

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-1999;

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RESULT 13
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21 OCT 1999
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9908-0161361
9908-0161361
9908-0161361
9908-0161361
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Pred. No. 3.9;
8; Mismatches
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11-APR-1999
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04-JUN 1999
07-JUN 1999
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07-WAY 1999

11-WAY-1999

14-WAY 1999

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18-WAY-1999

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99US-0142977 99US-0143542

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RESULT
G54042
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Best Local Similarity 36.2%;
Matches 17; Conservative
    25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G54042 standard; Protein;
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13-OCT-1999;
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22-JUL-1999 22-JUL-1999 22-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 02-AUG-1999 02-AUG-1999 03-AUG-1999 04-AUG-1999 04-AUG-1999 05-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 06-AUG-1999 09-AUG-1999

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20-AUG-1999 20-AUG-1999 20-AUG-1999 23-AUG-1999 23-AUG-1999 25-AUG-1999 26-AUG-1999 27-AUG-1999

7-AUG-18-AUG-

12-AUG 13-AUG 13-AUG

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Score 68.5; DB Pred. No. 6.5; 8; Mismatches
                 21;
                Length
                  350;
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Qy 2 SFPKYKPSSLRTLPETLDPAEYN-ISPETRRAQAERLAIRAQLKREY 47 :|||:||:|| :|| || 1 || 296 afpkwkptdletfvpnldpdgvdllskmllmdptkrinaraalehey 342

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Gaps

Search completed: April 29, 2001, 06:45:09 Job time: 625 sec

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US-08-750-717-2
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1 US-08-764-100-26 3 US-08-622-277A-8 1 US-08-6440-523B-32 US-08-440-845D-6 2 US-08-868-458-6 2 US-08-96-982-1 1 US-08-96-982-1 1 US-08-96-97-90-4 2 US-08-149-203A-9 1 US-08-149-203A-9 1 US-08-149-203A-9 2 US-08-892-770-6 2 US-08-892-770-5 4 US-09-978-347A-2 1 US-09-978-347A-2	3033	673	571	565	385	325	325	325	262	1382	793	716	362	362	362	379	1261	+
US-08-764-100-26 US-08-622-277A-8 US-08-64-523B-32 US-08-440-845D-6 US-08-866-982-1 US-08-966-982-1 US-08-965-570-4 US-08-965-570-4 US-08-142-473A-9 US-08-469-203A-9 US-08-469-203A-9 US-08-88-92-770-6 US-08-892-770-5 US-08-892-770-5 US-09-07-925-695-8	ب	4	N	2	2	ш	_	_	Ν	ω	L	2	4	2	ш	w	Н	
	US-07-925-695-8	US-09-078-347A-2	US-08-892-770-5	US-08-892-770-6	US-08-605-106-14	US-08-469-203A-9	US-08-469-203A-9	US-08-142-473A-9	US-08-719-697-10	US-09-057-570-4	US-08-015-985-3	US-08-766-982-1	US-08-868-458-6	US-08-440-845D-6	US-08-464-523B-32	US-08-622-277A-8	US-08-764-100-26	
82561999143166382 8256199914316638	Appl	Appl	, Appl	, Appl	1, App	, Appl	, Appl	, Appl	10, Appl	Appl	, Appl	, Appli		Appl	32, App	Appl	e 26, App.	

ALIGNMENTS

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US-08-785-065-3
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US-08-785-065-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                        TOPOLOGY: linea
IMMEDIATE SOURCE:
LIBRARY: Consen
                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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MEDIUM TYPE: Disacci
MEDIUM TYPE: IBM Compatible
DOS
                                                                                                                                                                                                                                                NAME: Billings, Lucy J
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: Herew
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CITY: Palo Alto
                 CLONE:
                                                                               STRANDEDNESS:
                                                                                                                                                                  TELEX:
                                                                                                                                                                                TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                LENGTH:
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                                                                                                amino acid
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                 Consensus
                                                                                                              129 amino acids
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                                Consensus
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                                                               linear
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Query Match

100.0%;

Score 678;

DB 2;

Length 129;

Best Local Similarity Matches 129; Conserv

Conservative

100.0%; Pred. No. 8.7e-75; tive 0; Mismatches 0;

Indels

0;

Gaps

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B. 9
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                                                          Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,065
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
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                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uence
                                                                                                                                         LIBRARY: Ger
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                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSEPKYKPSSLRTLPETLDPAEYNISPETRRAQAERLAIRAQLKREYLLQYNDDNRRGLI 60
LDRTFHLSY 129
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                                                                                                                                                                                                                          129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3174 Porter Drive
                                                         Conservative
                                                                                                                                                         GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bandman, Olga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette
                                                                                                                                                                                                 single
                                                                    75.8%;
73.6%;
                                                                                                                                                                                                                                                       10:
                                                         18;
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                                                      Score 514; DB 2;
Pred. No. 6.5e-55;
8; Mismatches 16;
                                                                                Length 129;
                                                      Indels
                                                      0;
                                                   Gaps
                                                    0;
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US-09-093-522-26

Sequence 26,

6, Application US/09093522 6015700

Patent No. 6015700 GENERAL INFORMATION:

APPLICANT:
APPLICANT:

APPLICANT:

Gustafson, Michael Limper, Andrew Leof, Edward B. Thomas, Charles F

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                                                                     Matches
                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26,
                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                         NAME: Ellinger, Mark S.
REGISTION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
240 AFPKWQAQDLATIVPTLDPAGLDLLSKMLRYEPNKRITARQALEHEY 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                y Match 10.3%;
Local Similarity 36.2%;
hes 17; Conservative
                                                                                                                                                                               STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 LDRTFHLSY 129
                                                                                                                                                                                                                TYPE:
                    2 SFPKYKPSSLTTLPETLDPAEYN-ISPETRRAQAERLAIRAQLKREY 47 : | | : | | : | | : |
                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 13-JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDRTFNISY 129
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                                                                                                                                                                                                          amino acid
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                                                                                                                                                                                                                      294 amino acids
                                                                                                                                                                                                                                                                                            612-288-9696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leof, Edward B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARINII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
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                                                                                                                                                                                                                                                            26:
                                                              Score 69.5; DB 2;
Pred. No. 1.4;
9; Mismatches 20;
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                                                                 20;
                                                                                              Length 294;
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Query Match
Best Local Similarity
Matches 17; Conserv
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TITLE OF INVENTION:
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                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein -093-522-26
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APPLICATION NUMBER: 08/8:
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    738-000-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 AFPKWQAQDLATIVPTLDPAGLDLLSKMLRYEPNKRITARQALEHEY 286
                                                                                                                                                                                                                                                                                                                                                                         STATE: New Total
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                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION
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                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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CLASSIFICATION:
                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SFPKYKPSSLRTLPETLDPAEYN-ISPETRRAQAERLAIRAQLKREY 47 :|||: | |: | |: | |: | |: ||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Continental Plaza
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Pred. No. 1.4;
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Best Local
                                                   Matches
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                                                                                  Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                   APPLICATION NUMBER: G
FILING DATE: 26-MAY-1
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                     MOLECULE TYPE:
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                                                 Local Similarity hes 29; Conserv
35 ERLAIRAQLKREYLLQYNDPNRRGLIENPALLRWAYARTINVYPNFRPTPKNSLMGALCG 94 | | | | | | | | : | : | : |
                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
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ZIP: 0760
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                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                   Conservative
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                                                                  10.2%; Score 69; DB 28.7%; Pred. No. 4.8;
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                                                                                DB 3;
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                                                 32; Indels 26;
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TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-644-372-2
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                                                                                                                                                                            Sequence 1, Application US/08946528 Patent No. 5958746
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                                                                                                                                                                 GENERAL INFORMATION:
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                                                           NUMBER OF SEQUENCES: SCORRESPONDENCE ADDRESS:
                                                                               APPLICANT: Corley, Neil C.
TITLE OF INVENTION: ELECTRON TRANSPORT PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202)861 3000
TELEPAX: (202)822-0944
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                  ADDRESSEE:
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS: ADDRESSE: CUSHMAN, DARBY & CUSHMAN

STREET: 1615 L. Street, N.W.
                                                                                                                                                                                                                                                                             59 LIENPALLRWAYARTINWYPNFRPTPKNSLMGALCGFGPLIFIYYIIKTERDRKEKL 115
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                                                                                                                                                                                                                                                                                                          44 PDVVSTAPTKLVNVSYNNLTVNLGNELTPTQVKNQPTKVSWDAEPGALYTLVMTDPDAPS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lazzeri, Mario E. APPLICANT: Nutman, Thomas B. APPLICANT: Weiss, Niklaus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 19910: CLASSIFICATION: 43:
                                                                                                                                                                                                                                                                                                                                       8 PSSLRTLPETLDPAEYN-----ISPETRRAQAERLAIRAQLKREYLLQYNDPNRRG 58
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                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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5. 5416009
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                          : Incyte Pharmaceuticals, Inc
3174 Porter Dr.
                                                                                                                                 Bandman, Olga
                                                                                                                                           Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No.
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                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MOORMANN,
APPLICANT: VAN RIJN,
TITLE OF INVENTION:
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Best Local (
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                        tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 305 amino acid
                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                     NUMBER OF SEQUENCES:
                                                              CITY: Arlington
STATE: Virginia
                                                                                             STREET:
                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                     265 HLPAPGDDVLVLLCGPPPMV 284
                                                                                                                                                                                                                                                                                                                                                                                    206 TQCFLLFANQTEKDIILREDLEELQARYPNRFKLWFTLDHPP-KDWAYSKGFVTADMIRE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                           149 PSGLLTY---TGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGITPMLQLIRAILKVPEDP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                 80 FRPTPKNSLMGALCGFGPLI 99
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SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 PSSLRTLPETLDPAEYNISPETRRAQAERLA-----IRAQLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/946,528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304
                                                                                                                                                                                                                                                                  2,
                                                                                                                                                                                                                                                                                                                                                                                                               79 TENPALLRWAYAR---TINVYPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
34; Conserv
                                                                                                                                                                                                                                                                Application US/08750717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                  745 South 23rd Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : PROSNOT16
1709102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                        YOUNG & THOMPSON
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                                                                                                                                                       Strains, Polypeptides Enco
Thereof for Diagnosis and
                                                                                                                                                                                Nucleotide Sequences of Pestivirus
                                                                                                                                               Infections
                                                                                                                                                                                                                    Robertus J. M.
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Pred. No. 6
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6.9;
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                                                                                                                                                 se Sequences and Use of Pestivirus
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CURRENT APPLICATION DATA:

PatentIn Release #1.0, Version #1.30

US/08/750,717

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

COMPUTER:

APPLICATION NUMBER: OPERATING SYSTEM: SOFTWARE: Patent:

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2311
                                                                                                                                                                                                                                                                                                                                                           ent No. 5910631
           SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US;08/605,106
FILING DATE: 23-SEPT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2261 ETGRALKQVVGLS------TAENALLVALFGYVGYQALSKRHIPVVTDIYSIEDHR- 2310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: V
FILING DATE: 16-JUN-
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                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                          -605-106-11
                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 RKEKLIQEGKLDRTFHLSY 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP 94201743.5 FILING DATE: 17-JUN-1994
                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                              COUNTRY: U
ZIP: 55402
                                                                                                                                                                             STREET: P.O. Box
CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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TELEX: 248425 EMBON
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                                                                                                          MEDIUM TYPE: Diskette
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CLASSIFICATION:
                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                             Application US/08605106
                                                                                                                                                                                                           E: Schwegman,
P.O. Box 2938
                                                                                                                                                             USA .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3898 amino acids
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                                                                                                                                                                                                                           Lundberg, Woessner & Kluth, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -PLIFIYYIIKTERD 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
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US-08-370-225-32
; Sequence 32, Applicati
; Patent No. 5580736
; GENERAL INFORMATION:

Application US/08370225

APPLICANT:

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                                                                                                                                                                                                                  ; TYPE: PRT ; ORGANISM: rhodopseudomonas sphaeroides US-09-587-066-6
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US-09-587-066-6
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                                                                                                                                                                                                                                                               SOFTWARE: Pa
SEQ ID NO 6
LENGTH: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: LUNNEN,
                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/09587066 Patent No. 6210945
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Matches 13; Conserv
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                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2000-06-02
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/587,066
                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 01-MAR-1996
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142 KMIRLVNSRQVGVAPNHVP 160
                                                                83
                                                                                                                                Local Similarity
nes 23; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                             65 -LLRWAYARTINVYPNFRP 82
                                                                                               11 LRTLPETLDPAEYNISPETRRAQAERLAIRA-----QLKREYLLQYNDPNRRGLIENPA 64
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                                                              IATIPPHL-PANNSIVAARGAGYPDRLFVSGATRHCMEFKATSNWQDGDPNRRVLTSAPT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Woessner, Warren
                                                                                                                                                                                                                                                                                                                                                                                              WILSON, GEOFFREY G.
VENTION: METHOD FOR CLONING AND PRODUCING THE RESTRICTION
VENTION: ENDONUCLEASE IN E. COLI AND PURIFICATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MORGAN, RICHARD D. MEIXSELL, TIMOTHY
                                                                                                                                Conservative
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                                                                                                                                                9.1%;
29.1%;
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                                                                                                                              10;
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                                                                                                                                                Score 62;
Pred. No.
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Pred. No. 1
                                                                                                                                Mismatches
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                                                                                                                                                                 Length 214;
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                                                                                                                              Gaps
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US-08-461-859-32
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US-08-370-225-32
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Best Local Similarity 29.1
                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/08461859
ZIP: 02110-200.

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

*COMPUTER: IBM PS/2 Model 50Z or 55SX

*COMPUTER: MS-DOS (Version 5.6)

**COMPUTER: MS-DOS (Version 5.1)
                                                                                                                                                                                                                                                                                               APPLICANT: Brent, Roger
                                                                                                                                                                                                                                                                                                                               tent No. 5786169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/143001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,225
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ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                          FITLE OF INVENTION:
                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 10/30/92 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (UE
TELEFAX: 200154
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                                                                                                        COUNTRY:
                                                                                                                          CITY: Boston
STATE: Massa
                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                             13 FPRVNPKGIDLLQRMLVFDP------AKRITAKEALEHPYLQTYHDPN 54
                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 FPKYKPSSLRTLPETL--DPAEYNISPETRRAQAERLAIRAQLKREYLLQYNDPN 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                          225 Franklin Street
                                                                                                                                                                                                                                                           Gyuris, Jeno
Golemis, Erica
                                                                                                            U.S.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                          Fish & Richardson P.C
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No. 5786169el Proteins
35
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29.1%;
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Pred. No. 1.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
APPLICATION NUMBER: 07/969,03
FILING DATE: 10/30/92
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELECHONE: (617) 542-5070
TELECHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                             COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: Wordperfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                              ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Interaction Traction of Invention: Novel Proteins Number of Sequences: 33
                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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LENGTH: 60
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TELEPHONE: (617) 542-5070
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                                                                                                                                                                                           APPLICATION NUMBER: PCT/US93/10069 FILING DATE: 20-OCT-1993
                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                    225 Franklin Street
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Number: 35,238
Number: 00786/143002
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January 9, 1995
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                                                                                                                                        07/969,038
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                                                      00786/143001
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Pred. No. 1.6;
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US=08-176-620A-14
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                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.1%;
Best Local Similarity 29.1%;
Matches 16; Conservative
                                                           Query Match 9.1
Best Local Similarity 29.1
Matches 16; Conservative
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PRIOR : PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                 TOPOLOGY: ur
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275 FPRVNPKGIDLLQRMLVFDP------AKRITAKEALEHPYLQTYHDPN 316
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/176,620A FILING DATE: 03-JAN-1994 CLASSIFICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 FPRVNPKGIDLLQRMLVFDP------AKRITAKEALEHPYLQTYHDPN 54
                                                                                                                                                                                                                TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                 3 FPKYKPSSLRTLPETL--DPAEYNISPETRRAQAERLAIRAQLKREYLLQYNDPN 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boulton, Teri G. Cobb, Melanie H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                             .Score 61.5; DB 1; Pred. No. 17; 7; Mismatches 17
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                                                                                              Length 353;
                                                               Indels
                                                               15;
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                                                               Gaps
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Search completed: April 29, 2001, 06:46:00 Job time: 311 sec